

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 8, 2006, 09:27:07 ; Search time 231 Seconds  
(without alignments)  
1212.531 Million cell updates/sec

Title: US-10-650-467-105  
Perfect score: 2074  
Sequence: 1 MVSSAATISTITSTTPSTPI.....QLHDLPTSTHSDRCAGNSF 397

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2074	100.0	397	2	Q9N4R5	CAEEL
2	1899	91.6	433	2	Q6F3C9	CAEEL
3	1768.5	85.3	444	2	Q625Z7	CAEEL
4	607.5	29.3	450	2	Q23305	CAEEL
5	529	25.5	600	2	Q9VW75	DROME
6	518.5	25.0	375	2	Q629B2	CAEEL
7	514	24.8	468	2	Q62062	CAEEL
8	495.5	23.9	470	2	Q7Q0B9	ANOAGA
9	487.5	23.5	453	2	Q618Q8	CAEEL
10	485.5	23.4	457	2	Q18534	CAEEL
11	462	22.3	430	2	Q810L4	CAEEL
12	461.5	22.3	365	2	Q9XXU4	CAEEL
13	461	22.2	362	2	Q6EUU1	CAEEL
14	460.5	22.2	387	2	Q22188	CAEEL
15	458	22.1	402	2	Q20275	CAEEL
16	456.5	22.0	404	2	Q611A4	CAEEL
17	433	20.9	266	2	Q61W82	CAEEL
18	432	20.8	492	2	Q6V1R1	SCHMA
19	421.5	20.3	402	2	Q964E5	DUGTI
20	390.5	18.8	375	2	Q57463	BRARE
21	386	18.6	370	1	GPRI0	HUMAN
22	386	18.6	370	2	Q5VXR9	HUMAN
23	386	18.6	370	2	Q502U8	HUMAN
24	385.5	18.6	370	2	Q6VNM6	MOUSE
25	384	18.5	377	2	Q8QGM3	CHICK
26	383	18.5	377	2	Q6LSJ7	CAEEL
27	382	18.4	376	2	P90745	CAEEL
28	379	18.3	481	2	Q7KFF8	DROME
29	379	18.3	485	2	Q9VNM1	DROME
30	378	18.2	316	2	Q60UD5	CAEEL
31	378	18.2	485	2	Q8S235	DROME

32	373.5	18.0	370	1	GPRI0	RAT
33	373.5	18.0	374	2	Q9YHX1	GADMO
34	372	17.9	400	2	Q7PQN7	ANOAGA
35	372	17.9	425	2	Q5QGM5	ANOAGA
36	371	17.9	339	2	Q4SRZ3	TETNG
37	369.5	17.8	396	2	Q50115	FUGRU
38	368	17.7	434	2	Q59883	CAEEL
39	367.5	17.7	427	2	Q9N324	CAEEL
40	367.5	17.7	438	2	Q615K7	CAEEL
41	366.5	17.7	370	2	Q4EW11	BOVIN
42	364.5	17.6	371	1	NPY6R	RABIT
43	363	17.5	372	2	Q6PR57	BRARE
44	361.5	17.4	354	2	Q50113	FUGRU
45	360.5	17.4	369	2	Q50114	FUGRU

ALIGNMENTS

RESULT 1  
Q9N4R5 CAEEL  
ID Q9N4R5 CAEEL PRELIMINARY; PRT; 397 AA.  
AC Q9N4R5;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=Y58G8A.4;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RG The C. elegans sequencing consortium;  
RT "Genome sequence of the nematode C. elegans: a platform for  
investigating biology."  
RL Scienc 284:2017-2018(1998).  
CG 1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
DR EMBL; AC006808; AAF60815.3; -; Genomic DNA.  
DR Wormbase; WBGene00021983; Y58G8A.4.  
DR WormPep; Y58G8A.4a; CE33345.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; P:receptor activity; IEA.  
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor activity; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm 1; 1.  
DR PRINTS; PR00237; GPCR\_RHODOPSIN.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Complete proteome; G-protein coupled receptor; Hypothetical protein;  
Receptor; Transducer; Transmembrane.  
SQ SEQUENCE 397 AA; 44536 MW; 092E3CAC4E765F81 CRC64;

Query Match	100.0%;	Score 2074;	DB 2;	Length 397;
Best Local Similarity	100.0%;	Pred. No. 3.2e-149;	Mismatches 0;	Gaps 0;
Matches 397;	Conservative 0;	Indels 0;	Gaps 0;	
QY	1	MVSSAATISTITSTTPSTISNVITSHNNGSCIQIAEALAAQGGDDITVDYFYSIFTF 60		
Db	1	MVSSAATISTITSTTPSTISNVITSHNNGSCIQIAEALAAQGGDDITVDYFYSIFTF 60		
QY	61	LYGFLFVLGIFGNGVLWAVARNKELQARNVFLNLFTDLILVFTAIPTVPTWAMTKD 120		
Db	61	LYGFLFVLGIFGNGVLWAVARNKELQARNVFLNLFTDLILVFTAIPTVPTWAMTKD 120		
QY	121	WAFGVMCHLPLNSCSVFVTSWLSLTALSLDKFLHNDPTKQPVYSIQALAITFLIV 180		
Db	121	WAFGVMCHLPLNSCSVFVTSWLSLTALSLDKFLHNDPTKQPVYSIQALAITFLIV 180		

11 Dec. 1998

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QY 181 STLINPILMSFEHVDGSPYVQGETPYCGHFCDEANWQSENRSKIYGTITVMLLQFVVPM 240
DB 181 STLINPILMSFEHVDGSPYVQGETPYCGHFCDEANWQSENRSKIYGTITVMLLQFVVPM 240
QY 241 AVITYCYFKILQKVSXDMIIQNAQFCQSLTKQKSDATSRKKKNYILIANVVTFIGCWL 300
DB 241 AVITYCYFKILQKVSXDMIIQNAQFCQSLTKQKSDATSRKKKNYILIANVVTFIGCWL 300
QY 301 PLTLNLVKDPKCEPEWMLKQPFPAWNAHVIAVMSLVVWNPFLPFWLTRKQKRSGLSKIL 360
DB 301 PLTLNLVKDPKCEPEWMLKQPFPAWNAHVIAVMSLVVWNPFLPFWLTRKQKRSGLSKIL 360
QY 361 NSTGSKKAGSGLRGIGLHLLPTSTHSDRCAGNSP 397
DB 361 NSTGSKKAGSGLRGIGLHLLPTSTHSDRCAGNSP 397

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## RESULT 2

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ID Q6F3C9 CAEL PRELIMINARY; PRT; 433 AA.
AC Q6F3C9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Y58G8A.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
RL Science 282:2012-2018 (1998).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AC068808; AAT6889.1; -; Genomic DNA.
DR Ensembl; Y58G8A.4; Caenorhabditis elegans.
DR WormBase; WBGene0021983; Y58G8A.4.
DR WormPeP; Y58G8A.4b; CE35962.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Complete proteome; G-protein coupled receptor; Hypothetical protein;
Receptor; Transducer; Transmembrane.
SQ SEQUENCE 433 AA; 48919 MW; 57D033P5PDDA70P5 CRC64;

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Query Match 91.6%; Score 1899; DB 2; Length 433;
Best Local Similarity 100.0%; Pred. No. 6.8e-136;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 MYSSAATISTITSTTTTPSTISNVIHSHNGSCIQIAEIAAAGIDDIIVDPIYSIFTF 60
DB 1 MYSSAATISTITSTTTTPSTISNVIHSHNGSCIQIAEIAAAGIDDIIVDPIYSIFTF 60
QY 61 LYGFPLVGIPIFGNGVLMVARNKRLQSAARNVFLNLIPTDLILVFTALPVPWYAMTKD 120
DB 61 LYGFPLVGIPIFGNGVLMVARNKRLQSAARNVFLNLIPTDLILVFTALPVPWYAMTKD 120
QY 121 WAFGSVMCHLVPLNSCSVFTVTSWLSLTAISLDKFLHNDPTKQPVSIROALAITFLIWI 180
DB 121 WAFGSVMCHLVPLNSCSVFTVTSWLSLTAISLDKFLHNDPTKQPVSIROALAITFLIWI 180

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QY 181 STLINPILMSFEHVDGSPYVQGETPYCGHFCDEANWQSENRSKIYGTITVMLLQFVVPM 240
DB 181 STLINPILMSFEHVDGSPYVQGETPYCGHFCDEANWQSENRSKIYGTITVMLLQFVVPM 240
QY 241 AVITYCYFKILQKVSXDMIIQNAQFCQSLTKQKSDATSRKKKNYILIANVVTFIGCWL 300
DB 241 AVITYCYFKILQKVSXDMIIQNAQFCQSLTKQKSDATSRKKKNYILIANVVTFIGCWL 300
QY 301 PLTLNLVKDPKCEPEWMLKQPFPAWNAHVIAVMSLVVWNPFLPFWLTRKQKRSGLSKIL 360
DB 301 PLTLNLVKDPKCEPEWMLKQPFPAWNAHVIAVMSLVVWNPFLPFWLTRKQKRSGLSKIL 360
QY 361 NSTE 364
DB 361 NSTE 364

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## RESULT 3

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ID Q625Z7 CAEBR PRELIMINARY; PRT; 444 AA.
AC Q625Z7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG01072.
GN Name=CBG01072;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
NUCLEOTIDE SEQUENCE.
RG The C. briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; CAAC01000007; CAB58004.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Hypothetical protein; Receptor;
Transducer; Transmembrane.
SQ SEQUENCE 444 AA; 50089 MW; B1794980E7DFC16A CRC64;

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Query Match 85.3%; Score 1768.5; DB 2; Length 444;
Best Local Similarity 91.0%; Pred. No. 5.7e-126;
Matches 342; Conservative 11; Mismatches 10; Indels 13; Gaps 2;

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```

QY 2 VSSAATISTIST-----TTPTSTISNVI-----TSHSNNGSCIQIAEIAAAGIDDI 48
DB 1 MTSSAVLHPISITISSTISPTISHTSHVITTTQSTSSQNNGTCTQIAEIAAAGIDDI 60
QY 49 TVDFYIRIFPLVGIPIFGNGVLMVARNKRLQSAARNVFLNLIPTDLILVFTA 108
DB 61 TVDFYIRIFPLVGIPIFGNGVLMVARNKRLQSAARNVFLNLIPTDLILVFTA 120
QY 109 IPTVTPWYAMTKDWFSGVMCHLVPLNSCSVFTVTSWLSLTAISLDKFLHNDPTKQPVSI 168
DB 121 IPTVTPWYAMTKDWFSGVMCHLVPLNSCSVFTVTSWLSLTAISLDKFLHNDPTKQPVSI 180
QY 169 QALAITFLIWIIVSTLINPILMSFEHVDGSPYVQGETPYCGHFCDEANWQSENRSKIY 228
DB 181 QALGITSLSIWIIVSTLINPILMSFEHVDGSPYVQGETPYCGHFCDEANWQSENRSKIY 240
QY 229 TTVMLLQFVVPMNAVITYCYFKILQKVSXDMIIQNAQFCQSLTKQKSDATSRKKKNYIL 288
DB 241 TTVMLLQFVVPMNAVITYCYFKILQKVSXDMIIQNAQFCQSLTKQKSDATSRKKKNYIL 300

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QY 289 IAMVTFICGWLPLTLNLVKKPEWIKROPPFWAINAHVIAVSNPLVWPLFFWLT 348
Db 301 IAMVTFICGWLPLTLNLVKKPEWIKROPPFWAIVAHVIAVSNPLVWPLFFWLT 360
QY 349 RKQKSGLSKILNSTE 364
Db 361 RKQKSGLSKILNSTE 376

RESULT 4
Q23305 CABEL
ID Q23305 CABEL PRELIMINARY; PRT; 450 AA.
AC Q23305;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE Hypothetical protein ZC412.1.
GN ORFNames=ZC412.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; Z78067; C801528.2; -; Genomic_DNA.
DR FIC; T27559; T27559.
DR Ensembl; ZC412.1; Caenorhabditis elegans.
DR WormBase; WBGene0013883; ZC412.1.
DR WormPep; ZC412.1; C835920.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR000611; NPY_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01012; NRPEPTIDEVR.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Complete proteome; G-protein coupled receptor; Hypothetical protein;
KW Receptor; Transducer; Transmembrane.
SQ SEQUENCE 450 AA; 51887 MW; 428608D8E26BF5C1 CRC64;

Query Match 29.3%; Score 607.5; DB 2; Length 450;
Best Local Similarity 35.3%; Pred. No. 8.5e-38;
Matches 119; Conservative 76; Mismatches 111; Indels 31; Gaps 7;

QY 33 CIOAEALAAAGQIDITVDYFIRSYFLYGLFVLGFGNGVLMVARNKRLQSRNV 92
Db 9 CIDVNAUL--QOFNDWTVFLFVRGLGYSVLFLIILIGLVGNLLITSILMRKGL-SVANI 65
QY 93 PLLNLIFDILVFTAIPTVPYAWTKDQAFGVSVMCHLVPLNSGCVFVTSLSLTSLD 152
Db 66 FLINLAVSDLLLCITAVDITPVLAFMKRWIRGIIMCKLVPTCOAFSVLSSWSLCTAID 125
QY 153 KFLINIDPTKQPSVIRQNALATFLIWIIVSTLINPLMSFPHVDGSPVYQGET----- 206
Db 126 YRISIVTFLRPPWDRHARWLIMFTWVVAFLASVPL-----YYSQNLKTMVENV 175
QY 207 PYCGHFDCEANQWQSENSRKI-YGVTVMLQFVPMNAVITYCFVKILQKVSXDMILIQNAQF 265
Db 176 TLCDGFCGFQWQDEISKLTYTYSLLIIQLIIPAIMSFICYLMLLQKVTQDVLDEGSM 235
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QY 266 COSLTQKQKSDATSRRKKVNYILIAMVTFICGWLPLTLNLVKKPEW----- 317
Db 236 ---LTTAAQQAQTAVRKRRVMYVLLIWMVIVFMAWCPPLSAVNLFRDLGIMGEFQCQTVYKVL 292
QY 318 LKROPPFWAINAHVIAVSNPLVWPLFFWLTTRKQKRS 354
Db 293 MMDQMYFKLLNVHVIAVTSIVWNPVLYFWMKSRHRA 329

RESULT 5
Q9VW75 DROME
ID Q9VW75 DROME PRELIMINARY; PRT; 600 AA.
AC Q9VW75; Q9VW74;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, last annotation update)
DE CG7395-PA (GH23382p) (Neuropeptide F-like receptor).
GN Name=NPR76F; ORFNames=CG7395;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Labko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celnikier S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Friese E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
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Best Local Similarity 30.5%; Pred.No. 1.le-31;					
Matches 136; Conservative 76; Mismatches 154; Indels 80; Gaps 12;					
QY	6	ATISTITSTTTPST-----ISNVITSHSNNGSCIOIAEAAOAGID---DITVDFY 53	:	:	:
DB	2	ANLSWLSLTITTTSSSISTSQLPLVSTTNWSLTSPTGTSAILADVAASDEDRSGGIHNOF 61	:	:	:
QY	54	IRSIFFFLVGFLVGLIFGNQGVLMVARNKRLOSARNVLLNLIFTDLLLVTAIPVTP 113	:	:	:
DB	62	VQIFFVLVLYATVPVLGVFGNVLCYYVLRNRAMQTVTNFIPTNLALSDIILLCLVLAVFPFP 121	:	:	:
QY	114	WYAWTKDMAFGSVMCHLVPLNSCSVFVTSWLSLTALSLOKFLHINDPDKPVSRQALAI 173	:	:	:
DB	122	LYTFMGRWAPGRSLCHLVSFQAQCSYISTLTLSAIDRYFVIYFFHPMKLSTCIGI 181	:	:	:
QY	174	TFLIWIVSTLINIPLYLMSFE-----HYDGSPYVOPG----- 204	:	:	:
DB	182	IVSIIWIALLATVPYGYMYKMNTNELVNGTGTNETLVTEATMLNGSFVAQSGGFIEAPDS 241	:	:	:
QY	205	-----ETPYCGHCDEANWOSENSRKLYGTVMLLQLFVPMVAITYC 246	:	:	:
DB	242	TSATQAYMQMTAGSTGPMPYRVYCEE--NWPSSEQYRKFVGAITTLQFVLPPFIISIC 300	:	:	:
QY	247	YFKILOKVSKDMIIONAQFCQSILTKQRSDA-TSRKKKNYILIAMVVTFIGCMPLTLTL 305	:	:	:
DB	301	YWVISVKLN-----QRAKPGSKSSREERDRKCTRMLIAMVAVELSWLPINVV 355	:	:	:
QY	306	NLVKDP-KCKPEWLKRGPPFWANAHVIANSLVVNPDLFPWLT---RKQRSGL----- 356	:	:	:
DB	356	NIFDDPDCKNEWRFYLFPFV--AHSIAMSSCTYNPFLYAWLNENFRIGPKFKHVLPFCNP 413	:	:	:
QY	357	--SKLNSTEGSKAGGSLRGLQLH 380	:	:	:
DB	414	SNNNIINTRTGYNKSDRNTC-GPRKH 438	:	:	:
RESULT 6					
ID	Q629B2	CABER PRELIMINARY; PRT; 375 AA.			
AC	Q629B2;				
DT	25-OCT-2004	(TrEMBLrel. 28, Created)			
DT	25-OCT-2004	(TrEMBLrel. 28, Last sequence update)			
DT	25-OCT-2004	(TrEMBLrel. 28, Last annotation update)			
DE	Hypothetical protein CBG00112 (Fragment).				
GN	Name=CBG00112;				
OS	Caenorhabditis briggsae.				
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdita; Rhabditoidea;				
OC	Rhabditidae; Peloderinae; Caenorhabditis.				
OX	NCBI_TaxID=6238;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RG	The C.briggsae Sequencing Consortium;				
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; CAAC01000002; CAB57235.1; -; Genomic DNA.				
DR	GO; GO:0016021; C:integral to membrane; IEA.				
DR	GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.				
DR	GO; GO:0004872; F:receptor activity; IEA.				
DR	GO; GO:0001584; F:rhopopsin-like receptor activity; IEA.				
DR	GO; GO:0007186; F:G-protein coupled receptor protein signalin. . ; IEA.				
DR	GO; GO:0007165; F:signal transduction; IEA.				
DR	InterPro; IPR000276; GPCR_Rhodpsn.				
DR	InterPro; IPR000611; NPY_Receptor.				
DR	Pfam; PF00001; 7tm_1.1.				
DR	PRINTS; PRO0237; GFERRHODOPSIN.				
DR	PRINTS; PR01012; NRPEPTIDEYR.				
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.				
DR	PROSITE; PS02362; G_PROTEIN_RECEP_F1_2; 1.				
KW	G-protein coupled receptor; Hypothetical protein; Receptor;				
KW	Transducer; Transmembrane.				
FT	NON_TER 1				
FT	NON_TER 375				
SQ	SEQUENCE 375 AA; 42616 MW; 341E2844A015659A CRC64;				

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila  
RT melanogaster euchromatic genome sequence.";   
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.M., Svirkas R.E.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RA "The transposable elements of the Drosophila melanogaster euchromatin:  
RT a genomics perspective.";   
RT Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RA "Annotation of the Drosophila melanogaster euchromatic genome: a  
RT systematic review.";   
RT Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RX Berkeley Drosophila Genome Project;  
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirkas R., Smith E.,  
RA Yu C., Rubin G.;  
RA "Drosophila melanogaster release 4 sequence.";   
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RX FlyBase;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RX STRAIN=Canton-S; TSSUB=Head;  
RA Peng G., Reale V., Chatwin H., Kennedy K., Venard Re., Ericsson C.,  
RA Yu K., Evans P.D., Hall L.M.;  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
DR EMBL; AE00514; AAF49074.2; -; Genomic\_DNA.  
DR EMBL; AY051588; AAK93012.1; -; mRNA.  
DR EMBL; AY192578; AAC39845.1; -; mRNA.  
DR Ensembl; CG7395; Drosophila melanogaster.  
DR FlyBase; FBgn0036934; CG7395.  
DR FlyBase; FBgn0036934; NPFR76F.  
DR GO; GO:0008188; F:neuropeptide receptor activity; IDA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR000611; NPY\_receptor.  
DR Pfam; PF00001; 7cm\_1; 1.  
DR PRINTS; PR00237; GPCKRHODOPSIN.  
DR PRINTS; PR01012; NRPEPTIDEYR.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Neuropeptide; Receptor; Transducer;  
KW Transmembrane.  
SQ SEQUENCE 600 AA; 66579 MW; E363BEF021BDA14B CRC64;



Query Match 25.0%; Score 518.5; DB 2; Length 375;  
Best Local Similarity 33.3%; Pred. No. 4.1e-311;  
Matches 113; Conservative 68; Mismatches 113; Indels 45; Gaps 7;  
QY 46 DDITVDVFYRSFTFLYGLFVLGIFGNGGVLMWAVARNKRLQSAARNVFLNLIIFTDLILV 105  
DB 18 EDMSTWYIMLFAFLYLIIAAGIIGNTCVILAITRNKALQTPVNLFILSLSCSDIVVC 77  
QY 106 FTAIPVTPYATKDAWAFSGVMCHLVPLNSCSGVFTWSLSLTAISLDKFLHNDPKQPV 165  
DB 78 CTSATITPTTAFKKEWIFGEVLCRVAPFIAGISLCSYFTLTAISIDRYILIRFPMPKPI 137  
QY 166 SIROALAITFLWIWSTLNLPLVMSFEHVDGSFVYQGETPYCGHFCDEANW-OSENSE 224  
DB 138 SHYQALGVIALCAPAATITSPIM--FKORLGEF-----ENFGUYCTE-NWGANESOR 188  
QY 225 KIYGTVMQLQFVPMNAVITYCYFKILQKVKMDIIONAQFQCSLTQKQKQSD----- 276  
DB 189 KIYGAALMFLQVLPITLIIISVTAISLKGQSMILKGA-----KKQKTDNWEIETSD 241  
QY 277 ----ATSRKKKKNYILIAMVVTFIGCWLPPLTLNLVQPKPEWIKRQFFFWAINAHVI 332  
DB 242 QORMAVKRRQRTNRMLGNWVAFACSWIWSVTFNILRDYELPDLIKNOEYIFGIATHCI 301  
QY 333 AMSLVVNNLLEF-----WLRKQKQKRS 355  
DB 302 AMTSTWNPLLYAVLNQLRAAFIDMLPQWLRRLNLDG 340

RESULT 7  
O62062\_CABEL PRELIMINARY; PRT; 468 AA.  
AC O62062;  
DT 01-AUG-1998 (TremBLrel. 07, Created)  
DT 01-AUG-1998 (TremBLrel. 07, Last sequence update)  
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)  
DE Hypothetical protein C16D6.2.  
GN ORFNames=C16D6.2;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Pelodermidae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RG The C. elegans sequencing consortium;  
RT "Genome sequence of the nematode C. elegans: a platform for investigating biology."  
RL Science 282:2012-2018(1998).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
DR EMBL; Z81472; CAB03888.2; -; Genomic\_DNA.  
DR PIR; T19340; T19340.  
DR Ensembl; C16D6.2; Caenorhabditis elegans.  
DR WormBase; WBGene0007635; C16D6.2.  
DR WormPep; C16D6.2; CE37317.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF000611; NPY\_receptor.  
DR Pfam; PF00001; 7tm 1; 1.  
DR PRINTS; PR00237; GPCRHHODPSN.  
DR PRINTS; PR01012; NRPEPTIDEYR.  
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; UNKNOWN 1.  
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.  
KW Complete proteome; G-protein coupled receptor; Hypothetical protein; Receptor; Transducer; Transmembrane.  
SQ SEQUENCE 468 AA; 52773 MW; 2A0F72C78E353D5 CRC64;

Query Match 24.8%; Score 514; DB 2; Length 468;  
Best Local Similarity 31.3%; Pred. No. 1.1e-30;  
Matches 114; Conservative 74; Mismatches 128; Indels 48; Gaps 9;  
QY 29 NNGSCIOAEATAAAGIDIDITVDVFYRSFTFLYGLFVLGIFGNGGVLMWAVARNKRLQ 88  
DB 2 NGSDCLNLSLWLYR-EDLSRWYIMLVFAFLYLIIAAGIIGNSCVILATRNKSLQT 60  
QY 89 ARNVFLNLIIFTDLILVFTAIPTVTPYATKDAWAFSGVMCHLVPLNSCSGVFTWSLSLTA 148  
DB 61 VBNLFILSLSCSDIVVCCTSATITPTTAFKKEWIFGEALCRITAPFIAGISLCSFTTLTA 120  
QY 149 ISLDKFLHNDPKQPVSIROALAITFLWIWSTLNLPLVMSFEHVDGSFVYQGETPY 208  
DB 121 ISIDRYILIRFPMPKPIITHYQAVGIAICAFAPATITSPIM--FKQKGEF-----ENF 172  
QY 209 CGHFCDEANW-OSENSEKIYGTVMNAVITYCYFKILQKVKMDIIONAQFQ 267  
DB 173 CGQYCTE-NWGANESORKIYGAALMFLQVLPITLIIISVTAISLKGQSMILKGA----- 227  
QY 268 SLTQKQKQSD-----ATSRKKKKNYILIAMVVTFIGCWLPPLTLNLVQPKPE 315  
DB 228 ---KKQKTDNWEIETSDQORIAVKRRQRTNRMLGNWVAFACSWIWSVTFNILRDYELP 284  
QY 316 EWLKQKQFFFWAINAHVIMSLVWVNPILF-----FWLRKQKQKRS--LS 357  
DB 285 ELIKTQYIFGIATHCIAMTSTWNPLLYAVLNQLRAAFIDMLPQWLRRLNLDG 344  
QY 358 KILN 361  
DB 345 PLIN 348  
RESULT 8  
Q7Q0B9\_ANOGA PRELIMINARY; PRT; 470 AA.  
AC Q7Q0B9;  
DT 01-MAR-2004 (TremBLrel. 26, Created)  
DT 01-MAR-2004 (TremBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)  
DE ENSANGP0000011806 (Fragment).  
GN Name=GRNPY3; ORFNames=ENSANGG000000009317;  
OS Anopheles gambiae str. PEST.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;  
OC Anophelinae; Anopheles.  
OX NCBI\_TaxID=180454;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=PEST;  
RG The Anopheles gambiae Sequence Committee;  
RT "Anopheles gambiae re-annotation."  
RL Submitted (APR-2002) to the EMBL/GenBank/DBSJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=PEST;  
RG The Anopheles gambiae Sequence Committee;  
RL Submitted (APR-2004) to the EMBL/GenBank/DBSJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is preliminary data.  
DR EMBL; AAB01008986; EAA00213.1; -; Genomic DNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000611; NPY\_receptor.  
DR Pfam; PF00001; 7tm 1; 1.  
DR PRINTS; PR00237; GPCRHHODPSN.  
DR PRINTS; PR01012; NRPEPTIDEYR.

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DR PROSITE; PS00237; G PROTEIN RECP F1_1; UNKNOWN_1.
DR PROSITE; PS00262; G PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON TER 470
SQ SEQUENCE 470 AA; 51957 MW; B99EBDE9B505DC4D CRC64;

Query Match      23.9%; Score 495.5; DB 2; Length 470;
Best Local Similarity 27.3%; Pred. No. 2.9e-29;
Matches 121; Conservative 84; Mismatches 156; Indels 81; Gaps 13;

QY 5 AATISTSTTTPSTISNVITSHN-----NGSCIQIAEAAIAAQAQDITVDV----- 52
DB 14 AVTVAT-ATSPRAASLVLDHTEPLAGTIPPAALMPARVLPSPNATNLITLLELLR 72
QY 53 -----YRISFTFLYGLFVLGIFGNGVLMVARNKRLQSRNV 92
DB 73 PNSTVAPPNGDNDIIFSNKLVQIVFCVLYSSIFVLGVFGVNLVYCVVFRNKAMQTNTL 132
QY 93 FLNLIPFDLILVTAIPVTPYAMTKDMFGSVNCHLVPLNSCSVFTVTSLSLTSLD 152
DB 133 FITLAUSDILLCVLAVFTPSYTFMRNRWVFKLLCHTVLAQGSVYISTLTJTSIAID 192
QY 153 KFLHNDPTKQPSVIRQALATFLIWIIVSTLINLPY-----LMSFEHVDGSFYVQ 202
DB 193 RPFVLIYPFPRMKLSTCITIIVLWSPAIVWTPYGLYMKLHGVALNGTNDATGPL--- 249
QY 203 PGSTPYCGHFCDEANWQSENKRYIGTTVMQLQFVPMNAVITYCYFKILQKVSQDMIIQ 262
DB 250 -SSAMYC-----BELMPSEMRKTPSIVTSILOQFVLPFIIMAFYICVIRLNDRAATKP 303
QY 263 AQPCQSLQKQSDATSRKKVNYLIAMVTFIGCWLPLTLNLVQDKPKK-PWLRKQ 321
DB 304 G-----SKTSREEDRRDKKTRNRLISMVAIFGISWLPVLVNMCDNFSDINSRRFY 359
QY 322 PPFMAINARVAMSLVNMNPLFFMLT---RKQKASGL-----SKILNSTEGSKKAGSG 373
DB 360 LIFFI--AHLTAMSTCYNPFYLAWLNDNFKEFKQVLPDPSRGRAGTVGNGRAGGG 417
QY 374 LRGIQLHLLPTSTHSR-CAGNS 396
DB 418 WR-----SERTCNGNN 428

RESULT 9
Q61808 CABER PRELIMINARY; PRT; 453 AA.
AC Q61808
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG14540.
GN Name=CBG14540;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=62338;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; CAAC01000068; CAB6647.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodop.
DR InterPro; IPR000611; NPY_Receptor.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GFCRRHODOPN.

DR PRINTS; PR01012; NRPEPTIDEYR.
DR PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
DR PROSITE; PS00262; G PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Receptor; Hypothetical protein; Receptor;
Transducer; Transmembrane.
SQ SEQUENCE 453 AA; 52101 MW; 38A7FA01B1054A3D CRC64;

Query Match      23.5%; Score 487.5; DB 2; Length 453;
Best Local Similarity 30.5%; Pred. No. 1.1e-28;
Matches 118; Conservative 77; Mismatches 115; Indels 77; Gaps 11;

QY 58 FTFLYGLFVLGIFGNGVLMVARNKRLQSRNVFLNLIPFDLILVTAIPVTPYAM 117
DB 29 FLCVYIFLFLGIFGNTLIIVTCSYKALLSVQIFILNLAASDIMMCLSLPITNV 88
QY 118 TKMAGFQSVNCHLVPLNSCSVFTVTSLSLTSLD KFLHNDPTKQPSVIRQALATFLI 177
DB 89 YKNWYFGNLLCHLIPCIGISIFVCTPSLGAIALDRYLIVVRHTTFLSQRGAFLTILL 148
QY 178 WIYSTLINLPLVMSFEHVDGSFYVQGETPYCGHFCDEANWQSENKRYIGTTVMQLQFV 237
DB 149 WILSFVVTLPYAFNMQMIET-----EHLGCFCTE-KWESAKSRAYTMIVLQAQFV 201
QY 238 VPMNAVITYCY---FKILQKVSQDMIIQNAQFCQSL-----T 270
DB 202 LPPAVMAFCYSNIPSVLSKRAQTKIRKWVERTSALESSCAPPSHGLQEYENELNEFLDKQ 261
QY 271 QKQSDATSRKKVNYLIAMVTFIGCWLPLTLNLVQDKPKKPEWLKQPPF----- 324
DB 262 EKQKQRVQLQNRRTSILVTVMVFMGITLPHNVVSLIIEYD-----ETQSPFLRFGD 315
QY 325 -----WAIN--AHVIMSLVNMNPLFFMLT---RKQK-----SGL--- 356
DB 316 DYDISYLLNLFTHSIAMSNIVNPNVLAWLNPSPRQLVIKTYFQDRKSDRIINQTSLYK 375
QY 357 SKILN---STEGSKKAGSGLRLGIQLH 380
DB 376 QKMLNEAKNSNGRMKNGNSCLKERELN 402

RESULT 10
Q18534 CABEL PRELIMINARY; PRT; 457 AA.
AC Q18534
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Neuropeptide receptor family protein 1.
GN Name=npr-1; ORFNames=C39E6.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=93069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
RL Science 282:2012-2018 (1998).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; U49944; AA93419.1; -; Genomic DNA.
DR FIR; T29741; T29741.
DR WormBase; WBGen00003807; npr-1.
DR WormPep; C39E6.6; C39E6.6.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
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CC      O44820:F52C6.3; NBExp=1; IntrAct=EBI-318084, EBI-318098;
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC      EMBL; AL008868; CAAL5513.1; -; Genomic_DNA.
DR      PIR; T20184; T20184.
DR      HSRP; P02699; IL9H.
DR      INACT; O3XU4; -.
DR      Ensembl; C53C7.1; Caenorhabditis elegans.
DR      WormBase; WBGene0008278; C53C7.1.
DR      WormPep; C53C7.1b; CE36989.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      GO; GO:0004872; F:rhodopsin-like receptor activity; IEA.
DR      GO; GO:0001584; P:G-protein-coupled receptor activity; IEA.
DR      GO; GO:0007186; P:G-protein-coupled receptor protein signalin. .; IEA.
DR      GO; GO:0007165; P:signal transduction; IEA.
DR      InterPro; IPR000276; GPCR_Rhodopsn.
DR      InterPro; IPR000611; NPY_receptor.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCRHOPOPSN.
DR      PRINTS; PR01012; NRPEPTIDEYR.
DR      PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN 1.
DR      PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW      Complete proteome; G-protein coupled receptor; Hypothetical protein;
KW      Receptor; Transducer; Transmembrane.
SQ      SEQUENCE 365 AA; 40860 MW; 5DB21F7EBF5B89AF CRC64;

Query Match      22.3%; Score 461.5; DB 2; Length 365;
Best Local Similarity 30.9%; Pred. No. 8.4e-27;
Matches 110; Conservative 79; Mismatches 138; Indels 29; Gaps 8;

QY      28  SNNGSCIOAEIAAAGIDDDITVDYFIRSIPTFLYGLFVLGIFGNGGVLWAVARNKRLQ 87
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2  SSSNHCIDI-RAYLWQTKHDLTLHPITAILATIYTIIVVGVTGNLLVVMVMRFKVLQ 60
QY      88  SARNVFLNLIFTDLLIVFTAIPTVPMYAMTKDQAFGVMCHLVPLNSCSVFVTSWLSLT 147
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61  SVRNWFIVLSVSDIFVAIVSGSVTPITAFSKVWLFGGPLCHLLPLOGTALSFSFTLTIT 120
QY      148  AISLDKPLHNDPKQVSIROALAITFLIWTSTLINLPY-----LMSFEHVDGSFVYQ 202
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121  AIAIDRYILICHTKEPIRKQALNMISFNSAISVGLSVPLFMKQELMQFRN-----172
QY      203  PGETPYCHGFCDENWQSE-NSRKLYGTVMMLQFVPMVAVITYCYFKILQKVKDMIIQ 261
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
173  -----YCEYCSB-NWGPDAYLRSVYGVTFIIQFVPLTIITPCYASISIKLRGVFVR 226
QY      262  NAFQCSLTQKORSATSKKKVNYILIAMVVTFIGCMPLTLNLVKDFKKEPEWLRKQ 321
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
227  GSQ--KELMSEARRQLTQRLRTNRMLIIMTVTFALSMLPSVGFNPLRDYSALPGIDSQ 284
QY      322  PPFMAINAHVIAMSLVVMNPLFFWLTQKQKSGLSKILNSTEGSKAGGSLRGI 377
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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DT      25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE      Hypothetical protein C53C7.1b.
GN      ORFNames=C53C7.1, C53C7.1B;
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC      Rhabditidae; Peloderinae; Caenorhabditis.
OX      NCBI_TaxID=6239;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=Bristol N2;
RX      MEDLINE=99069613; PubMed=9851916;
RG      The C. elegans sequencing consortium;

*Genome sequence of the nematode C. elegans: a platform for
investigating biology.*;
Science 282:2012-2018(1998).
-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
EMBL; AL008868; CAH04724.1; -; Genomic DNA.
Ensembl; C53C7.1; Caenorhabditis elegans.
WormBase; WBGene0008278; C53C7.1.
WormPep; C53C7.1b; CE36989.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0004872; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001584; P:G-protein-coupled receptor activity; IEA.
GO; GO:0007186; P:G-protein-coupled receptor protein signalin. .; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
InterPro; IPR000611; NPY_receptor.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHOPOPSN.
PRINTS; PR01012; NRPEPTIDEYR.
PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN 1.
PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW      Complete proteome; G-protein coupled receptor; Hypothetical protein;
KW      Receptor; Transducer; Transmembrane.
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Best Local Similarity 31.3%; Pred. No. 9.1e-27;
Matches 108; Conservative 77; Mismatches 136; Indels 24; Gaps 7;

QY      28  SNNGSCIOAEIAAAGIDDDITVDYFIRSIPTFLYGLFVLGIFGNGGVLWAVARNKRLQ 87
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2  SSSNHCIDI-RAYLWQTKHDLTLHPITAILATIYTIIVVGVTGNLLVVMVMRFKVLQ 60
QY      88  SARNVFLNLIFTDLLIVFTAIPTVPMYAMTKDQAFGVMCHLVPLNSCSVFVTSWLSLT 147
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61  SVRNWFIVLSVSDIFVAIVSGSVTPITAFSKVWLFGGPLCHLLPLOGTALSFSFTLTIT 120
QY      148  AISLDKPLHNDPKQVSIROALAITFLIWTSTLINLPY-----LMSFEHVDGSFVYQ 202
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121  AIAIDRYILICHTKEPIRKQALNMISFNSAISVGLSVPLFMKQELMQFRN-----172
QY      203  PGETPYCHGFCDENWQSE-NSRKLYGTVMMLQFVPMVAVITYCYFKILQKVKDMIIQ 261
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QY      262  NAFQCSLTQKORSATSKKKVNYILIAMVVTFIGCMPLTLNLVKDFKKEPEWLRKQ 321
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
227  GSQ--KELMSEARRQLTQRLRTNRMLIIMTVTFALSMLPSVGFNPLRDYSALPGIDSQ 284
QY      322  PPFMAINAHVIAMSLVVMNPLFFWLTQKQKSGLSKILNSTEGS 366
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DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Hypothetical protein npr-2.
GN      Name=npr-2; ORFNames=T05A1.1, T05A1.1B;
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC      Rhabditidae; Peloderinae; Caenorhabditis.
OX      NCBI_TaxID=6239;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=Bristol N2;
RX      MEDLINE=99069613; PubMed=9851916;
RG      The C. elegans sequencing consortium;
RT      *Genome sequence of the nematode C. elegans: a platform for

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RT investigating biology";
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; Z68219; CAA92481.2; -; Genomic_DNA.
DR PIR; T24487; T24487.
DR Ensembl; T0SA1.1; Caenorhabditis elegans.
DR WormBase; WSGene0003808; npr-2.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004983; F:neuropeptide y receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR01012; NRPEPTIDEYR.
DR PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP F1_2; 1.
KW Complete proteome; G-protein coupled receptor; Hypothetical protein;
KW Receptor; Transducer; Transmembrane.
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Best Local Similarity 28.5%; Pred. No. 1.1e-26;
Matches 105; Conservative 80; Mismatches 118; Indels 65; Gaps 8;

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DB 18 DMNEPTVLVTFSLLYLHIFLLGLGNSAVLYLTKHROLQTVQNTFILNLCASNVLML 77

QY 107 TALFVTPWYANTKDWAFSGVMCHVPLNSCSVFVTSWLSLTALSLDKFLHNDPTQPV 166
DB 78 TSLPIFITNVYKQWFPSPVCKLPLVQGSIFVSTFSLAALDRYNLVVPHKQLS 137

QY 167 IQALAITFLIWTSLINLPY--LMSFEHVDGSGFYVQGETPYCGHFCDEANWQNSGR 224
DB 138 SRSANMIALLIWISVVVCMYPGYMDVEKLG-----LCGEYCSE-HWPLAEVR 186

QY 225 KIYGTVMLOFVVPNAVITYCYFKI-----LQKVS-KDMLIQNAQFC----- 266
DB 187 KGTEFLVLTQFLFPFATWAFACYNIFSRLRQVETKLLKLSRSOLLENSTTCGTNHI 246

QY 267 -----QSLTQKQSDATSRKKVNYILIAMVVTFIGMPLTLMLVLDKPKKEPW 317
DB 247 VSINAEAVQNGLENKQLAVLAQRRTTILSCWLLPFTWLPVHNVVTLMIY----- 300

QY 318 LKKQPFM-----AINAHVIAVMSLVVWNPPLFPWLTQRKQSGLSKILN 361
DB 301 ---DGFFHSDTSATSDHTYIVSMTHLISMLTNVTPFLYAWLNPMFKMLIKTLRG 357

QY 362 STEGSKKA 369
DB 358 GSKSPKPA 365

RESULT 15
Q02075 CAREL
ID Q02075; CABEL PRELIMINARY; PRT; 402 AA.
AC Q02075;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein F41E7.3.
GN ORFNames=F41E7.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]

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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology";
RL Science 282:2012-2018(1998).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; Z68106; CAA92126.2; -; Genomic_DNA.
DR PIR; T22076; T22076.
DR Ensembl; F41E7.3; Caenorhabditis elegans.
DR WormBase; WSGene00009619; F41E7.3.
DR WormPep; F41E7.3; CE31509.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004983; F:neuropeptide y receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000611; NPY_Receptor.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PRINTS; PR01012; NRPEPTIDEYR.
DR PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP F1_2; 1.
DR PROSITE; PS00626; RC1_2; UNKNOWN_1.
KW Complete proteome; G-protein coupled receptor; Hypothetical protein;
KW Receptor; Transducer; Transmembrane.
SQ SEQUENCE 402 AA; 46285 MW; 7DE92DA6E9AC523 CRC64;

Query Match 22.1%; Score 458; DB 2; Length 402;
Best Local Similarity 30.5%; Pred. No. 1.7e-26;
Matches 108; Conservative 77; Mismatches 109; Indels 60; Gaps 12;

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DB 8 SVSSILNETTPSYQST--CKIKNNPMEME-----YFRPFISMYCAVF 48

QY 67 VLGIPEGGVGVAVARNKRLQSANVPLNLITDILVLTALPVTWYANTKDWAFSGV 126
DB 49 LVASSGNFLVYVWVTNKMOTITNIFITNLAVSDIMVAFVTSIIGHWIFGGG 108

QY 127 MCHLVPLNSCSVFVTSWLSLTALSLDKF-----LHNDPTQPVSIQALAITFLI 177
DB 109 LCHGLPLFOGTSIFISTWTLTAIDRYIVIVHNSNININD----RMSRSCLSFTVLI 164

QY 178 WIVSTLINLPYL-----MSFEHVDGSGFYVQGETPYCGHFCDEANWQNSRKYIYGVML 233
DB 165 WLCSSLVLTVPYAINMKLNYIHEPCDFLI-----CSE-DWSNAEFSRISFGIVMI 212

QY 234 LQVVPVMAVITYCYFKILOKVKDMLIQNAQFCQSLTQKQSDATSRKKVNYILAMV 293
DB 213 LQFILFPLVLIATSYIKI-----WLFNSR--QSMTER--QSMTER--IKRKRLRLMLVWV 261

QY 294 FTIGCWLPVLTLLNVLKDKPEKPEWMLKQPFVAINAHVIAVMSLVVWNPPLFPWL 347
DB 262 IFAIWFPFNLNCLRDLDKLD-NFMRGYFSFVFLSVHLSMTATATAWNPLIYAFM 314

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GenCore version 5.1.8  
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(without alignments)  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- GenEmbl.\*  
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2: gb.in.\*  
3: gb.envi.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pr.\*  
9: gb.ro.\*  
10: gb.sts.\*  
11: gb.sy.\*  
12: gb.un.\*  
13: gb.vi.\*  
14: gb.hcg.\*  
15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1193	100.0	1193	6	AX151319 Sequence
3	1193	100.0	1500	6	AR408559 Sequence
4	1193	100.0	1500	6	AX151254 Sequence
5	1109	93.0	1301	6	AR408594 Sequence
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C 8	330	27.7	195349	14	AC006705 Caenorhab
9	96.6	8.1	1130	6	AR408550 Sequence
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15	69.8	5.9	1315	5	AF073925 Gadus mor
16	67.2	5.6	1303	2	AY579078 Anopheles
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ALIGNMENTS

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LOCUS	Sequence 104 from patent US 6632621.					
DEFINITION	Sequence 104 from patent US 6632621.					
ACCESSION	AR408593					
VERSION	AR408593.1	GI:40158833				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1193)					
AUTHORS	Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.					
TITLE	G protein-coupled receptor-like receptors and modulators thereof					
JOURNAL	Patent: US 6632621-A 104 14-OCT-2003;					
Pharmacia & Upjohn Company; Kalamazoo, MI						
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Db	61	AGCAACGTTATCAAGTCATTCGAACTGGCTCGTGCATTCAGATCGCTGAGGCGATT	120		
QY	121	GGGCACCAAGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC	180		
Db	121	GGGCACCAAGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC	180		
QY	181	CTCTACGGTTCCTGTTGTATTAGGCATTTTGGAAACGGGGCGGTACTATGGCGGTG	240		
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RESULT 2  
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DEFINITION Sequence 104 from Patent WO0138533.  
ACCESSION AX151319  
VERSION AX151319.1 GI:14533456  
KEYWORDS Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.  
TITLE G protein-coupled receptor-like receptors and modulators thereof  
JOURNAL Patent: WO 0138533-A 104 31-MAY-2001;  
PHARMACIA & UPJOHN COMPANY (US)  
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/db\_xref="GI:14533457"  
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CDS

Query Match 100.0%; Score 1193; DB 6; Length 1193;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Qy 241 GCGAGAACAGCGGCTCCAATCGGTCGCAACGATTTTCTGCTCAACTTCATCTTCAACC 300  
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ORIGIN

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RESULT 3
LOCUS AR408559
DEFINITION Sequence 39 from patent US 6632621.
ACCESSION AR408559
VERSION AR408559.1 GI:40158799
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1500)
TITLES Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.
JOURNAL G protein-coupled receptor-like receptors and modulators thereof
Patent: US 6632621-A 39 14-OCT-2003;
Pharmacia & Upjohn Company; Kalamazoo, MI
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/mol_type="genomic DNA"

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Query Match 100.0%; Score 1193; DB 6; Length 1500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 39 from Patent WO0138533.
ACCESSION  AX151254
VERSION     AX151254.1  GI:14533418
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homidae; Homo.
REFERENCE   1
AUTHORS    Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.
TITLE      G protein-coupled receptor-like receptors and modulators thereof
JOURNAL    Patent: WO 0138533-A 39 31-MAY-2001;
            PHARMACIA & UPJOHN COMPANY (US)
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ORIGIN
Query Match      100.0%; Score 1193; DB 6; Length 1500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      667  TGGGCATTCGGGTCACTGATGTCGCAATTTAGTTCCTTTGTCAAAATTCGGTTCGGGTGTT 726

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LOCUS      AR408594      1301 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 106 from patent US 6632621.
ACCESSION  AR408594
VERSION     AR408594.1  GI:40158834
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
            1 (bases 1 to 1301)
REFERENCE   Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.
AUTHORS    G protein-coupled receptor-like receptors and modulators thereof
TITLE      Patent: US 6632621-A 106 14-OCT-2003;
JOURNAL    Pharmacia & Upjohn Company; Kalamazoo, MI
FEATURES   Location/Qualifiers
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Query Match      93.0%; Score 1109; DB 6; Length 1301;
Best Local Similarity 94.2%; Pred. No. 0;
Matches 1193; Conservative 0; Mismatches 0; Indels 74; Gaps 1;

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LOCUS      1301 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 106 from Patent WO0138533.
ACCESSION  AX151321
VERSION     AX151321.1  GI:145333458
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.
  TITLE     G protein-coupled receptor-like receptors and modulators thereof
  JOURNAL   Patent: WO 0138533-A 106 31-MAY-2001;
            PHARMACIA & UPJOHN COMPANY (US)
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CDS
ORIGIN
Query Match      93.0%; Score 1109; DB 6; Length 1301;
Best Local Similarity 94.2%; Pred. No. 0;
Matches 1193; Conservative 0; Mismatches 0; Indels 74; Gaps 1;

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DB 121 GCGGCACAGGCATCGATGATATTTACTGTAGACCTTTTACATCCGATCAATCTTCAATTC 180
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DEFINITION Caenorhabditis elegans cosmid Y58G8A, complete sequence.  
ACCESSION AC006808  
VERSION AC006808.1 GI:4263130  
KEYWORDS HTG.  
SOURCE Caenorhabditis elegans  
ORGANISM Caenorhabditis elegans  
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Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.  
1 (bases 1 to 34544)  
C. elegans Sequencing Consortium  
Genome sequence of the nematode C. elegans: a platform for  
investigating Biology  
Science 282 (5396), 2012-2018 (1998)  
9851916  
2 (bases 1 to 34544)  
Tin-Mollam,A., Graves,T. and Harrison,M.  
The sequence of C. elegans cosmid Y58G8A  
Unpublished (2001)  
3 (bases 1 to 34544)  
Waterston,R.H.  
Direct Submission  
Submitted (23-FEB-1999) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
4 (bases 1 to 34544)  
Waterston,R.H.  
Direct Submission  
Submitted (01-MAR-2000) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
5 (bases 1 to 34544)  
Waterston,R.  
Direct Submission  
Submitted (28-MAR-2000) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
6 (bases 1 to 34544)  
Waterston,R.  
Direct Submission  
Submitted (03-NOV-2001) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, St.  
Louis, MO 63110, USA  
7 (bases 1 to 34544)  
Waterston,R.  
Direct Submission  
Submitted (29-MAY-2002) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63110, USA  
8 (bases 1 to 34544)  
Waterston,R.  
Direct Submission  
Submitted (07-JUN-2002) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63110, USA  
9 (bases 1 to 34544)  
Waterston,R.  
Direct Submission  
Submitted (22-NOV-2002) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63110, USA  
10 (bases 1 to 34544)  
Waterston,R.  
Direct Submission  
Submitted (24-JAN-2003) Department of Genetics, Washington



University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA  
11 (bases 1 to 34544)  
Wilson, R.  
Direct Submission  
Submitted (08-JUL-2004) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA  
12 (bases 1 to 34544)  
WormBase Consortium  
Direct Submission  
Submitted (22-SEP-2004) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA  
13 (bases 1 to 34544)  
WormBase Consortium  
Direct Submission  
Submitted (23-JUN-2005) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA  
Submitted by:  
Genome Sequencing Center  
Department of Genetics, Washington University  
St. Louis, MO 63110, USA, and  
Sanger Centre, Hinxton Hall  
Cambridge CB10 1RQ, England  
email: submissions@watson.wustl.edu and jesse@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone.

For a graphical representation of this clone sequence and its analysis see:  
<http://www.wormbase.org/db/seq/sequence?name=Y58G8A;class=Sequence>

#### NEIGHBORING CLONE INFORMATION

The 5' clone is R02C2, 3100 bp overlap; the 3' clone is F33E11, 200 bp overlap. Actual start of this clone is at base position 20847 of DC2; actual end is at 7365 of T22H9.

#### NOTES:

Coding sequences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara ([http://www.ddbj.nig.ac.jp/c-elegans/html/CE\\_INDEX.html](http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html)) and The C. elegans ORFeome cloning project (<http://worldb.dfci.harvard.edu/>), similarity to other proteins from Blastx analyses (<http://blast.wustl.edu/>), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program tRNAscan-SG (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).

#### FEATURES

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DEFINITION ***, 2 unordered pieces.
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AC006705.1 GI:4263233
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KEYWORDS Caenorhabditis elegans
SOURCE Caenorhabditis elegans
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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1 (bases 1 to 195349)
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2 (bases 1 to 195349)
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```
Unpublished
```

```
Waterston.R.H.
```

```
Submitted (23-FEB-1999)
```

```
University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
```

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* NOTE: This is a 'working draft' sequence. It currently
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* consists of 2 contigs. The true order of the pieces
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```
* is not known and their order in this sequence record is
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```
* arbitrary. Gaps between the contigs are represented as
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* runs of N, but the exact sizes of the gaps are unknown.
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* This record will be updated with the finished sequence
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* as soon as it is available and the accession number will
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* be preserved.
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* 1 52714: contig of 52714 bp in length
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VERSION AR408550.1 GI:40158790
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KEYWORDS
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SOURCE Unknown.
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ORGANISM Unknown.
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REFERENCE 1 (bases 1 to 1130)
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AUTHORS Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.
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TITLE G protein-coupled receptor-like receptors and modulators thereof
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JOURNAL Patent: US 632621-A 21 14-OCT-2003;
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Pharmacia & Upjohn Company; Kalamazoo, MI
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## RESULT 10

AX151236  
LOCUS AX151236 1130 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 21 from Patent WO0138533.  
ACCESSION AX151236  
VERSION AX151236.1 GI:145333400  
KEYWORDS

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.

## REFERENCE

1 Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.

## AUTHORS

TITLE G protein-coupled receptor-like receptors and modulators thereof  
JOURNAL Patent: WO 0138533-A 21 31-MAY-2001;  
PHARMACIA & UPJOHN COMPANY (US)  
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Query Match 8.1%; Score 96.6; DB 6; Length 1130;  
Best Local Similarity 47.0%; Pred. No. 1-2e-16;  
Matches 438; Conservative 0; Mismatches 454; Indels 39; Gaps 3;  
QY 136 GATGATATTTAGTGTAGACTTTTACATCCGATCAATCTTACATTCCTCTACCGGTTCTCGT 195  
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QY 841 AAGAGAAAGTGAATTATTTCTAATTCGAATGGTTGTGCATTTATCGGTTGGTTG 900
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Db 808 TGGTCAGTGACGTTCAACATTTCTGAGGACTATGATATTTGCCAGAGCTCATCAAACT 867
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Db 868 CAAGAATATATCTTTGGAAATGCTACACATTCGATTCGAATGACCTCAACGCTATGGAAC 927
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Db 928 CCGTTACTTACGCGAGTCTCAACCTCAAC 958

RESULT 11
LOCUS AR408557 1098 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 35 from patent US 6632621.
ACCESSION AR408557
VERSION AR408557.1 GI:40158797
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1098)
AUTHORS Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.
TITLE G protein-coupled receptor-like receptors and modulators thereof
JOURNAL Patent: US 6632621-A 35 14-OCT-2003;
Pharmacia & Upjohn Company; Kalamazoo, MI
FEATURES
Location/Qualifiers
source 1..1098
/organism="unknown"
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ORIGIN
Query Match 7.0%; Score 84; DB 6; Length 1098;
Best Local Similarity 50.5%; Pred. No. 6e-13;
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QY 167 CAATCTTCACTTCTACGGGTTCCCTGTTTGTATAGGCATTTTGGAAACGGCGG 226
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QY 227 TACTATGGCGGTGGCGAGAAACAGCGGCTCCAATCGGCTCGCAACGTAATTTCTGCTCA 286
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QY 287 ACTTGATCTTCAACGATTTGATATTTGGTGTTCACAGCGATTCAGTCACACCATGGTAGC 346
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RESULT 12

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AX151250
LOCUS AX151250 1098 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 35 from Patent WO0138533.
ACCESSION AX151250
VERSION AX151250.1 GI:14533414
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.
TITLE G protein-coupled receptor-like receptors and modulators thereof
JOURNAL Patent: WO 0138533-A 35 31-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
FEATURES
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ORIGIN
Query Match 7.0%; Score 84; DB 6; Length 1098;
Best Local Similarity 50.5%; Pred. No. 6e-13;
Matches 204; Conservative 0; Mismatches 200; Indels 0; Gaps 0;
QY 167 CAATCTTCACTTCTACGGGTTCCCTGTTTGTATAGGCATTTTGGAAACGGCGG 226
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RESULT 13
LOCUS AR408548 1352 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 15 from patent US 6632621.

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ACCESSION AR408548  
VERSION AR408548.1 GI:40158788  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1352)  
AUTHORS Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.  
TITLE G protein-coupled receptor-like receptors and modulators thereof  
JOURNAL Patent: US 632621-A 15 14-OCT-2003;  
Pharmacia & Upjohn Company; Kalamazoo, MI  
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Query Match 6.6%; Score 78.8; DB 6; Length 1352;  
Best Local Similarity 47.4%; Pred. No. 2.1e-11;  
Matches 381; Conservative 0; Mismatches 402; Indels 21; Gaps 4;  
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LOCUS AX151230  
DEFINITION Sequence 15 from Patent WO0138533.  
ACCESSION AX151230  
VERSION AX151230.1 GI:14533396  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.  
TITLE G protein-coupled receptor-like receptors and modulators thereof  
JOURNAL Patent: WO 0138533-A 15 31-MAY-2001;  
PHARMACIA & UPJOHN COMPANY (US)  
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ORIGIN  
Query Match 6.6%; Score 78.8; DB 6; Length 1352;  
Best Local Similarity 47.4%; Pred. No. 2.1e-11;  
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ACCESSION
  AF073925
VERSION
  AF073925.1 GI:4106396
KEYWORDS
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REFERENCE
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  Arvidsson,A.K., Wraith,A., Jonsson-Rylander,A.C. and Larhammar,D.
  Cloning of a neuroepitide Y/peptide YY receptor from the Atlantic
  cod: the Yb receptor
  Regul. Pept. 75-76, 39-43 (1998)
JOURNAL
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  9802392
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  2 (bases 1 to 1315)
  Arvidsson,A.-K., Wraith,A., Jonsson-Rylander,A.-C. and Larhammar,D.
  Direct Submission
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ORIGIN
Query Match      5.9%; Score 69.8; DB 5; Length 1315;
Best Local Similarity 45.0%; Pred. No. 9.5e-09;
Matches 263; Conservative 0; Mismatches 322; Indels 0; Gaps 0;

Qy 170 TCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTGGAAAGCGCGCGTAC 229
Db 187 TCCTCATCTCGTCTTACAGCACCATGATCGCGGTGGGATCGTGGGCACTCTTGCCTGG 246
Qy 230 TATGGGCGGTGGCGAGAAACAAGCGGCTCCAAATCGGCTCGCAACGTATTTCTGCTCAACT 289
Db 247 TCTTCGTATCGCCAGGAGGAGATGCAACAGTCAACCAACATCTTCATCGCAACC 306
Qy 290 TGATCTTCACCGATTTGATATTTGGTGTTCACAGGATTCAGATTCACCATGTTAGCGGA 349
Db 307 TGTCTGCTCGGACATCTCATGTGCTATCTTCTGCTGCGGTCACGCTCATCTACACCC 366
Qy 350 TGACCAAGACTCTGGGCATTCGGGTGAGTGATGTCCTATTTAGTTCTTGTCAAATTCGT 409
Db 367 TGATGGACCGCTGGATCTCTGGGGAGGCCCTGTGGAAGCTCACCCGTTCTGCGAGTGA 426
Qy 410 GTTCGGTGTGTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAAATTTCTGCATA 469
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Qy 470 TCAACGATCCCAACCAACACACGATTTCTATGTCGAAGCGTTGGCAATACATTTCTTA 529
Db 487 TCATCCACCCCAACGGGCTGGAAGCCCATGTCGGCCAGTCCCTACATGCGCGGTGGCATCA 546
Qy 530 TCTGGATAGTCTCAACACTGATAAATCTPACCGTATCTTATGTTCTTTTCGAGCAGCTGATG 589
Db 547 TCTGGTGGTGGCCCTGCGCTCATCTCCGTCCTTTCTCTGCTTTCACCGTGTGGACAACC 606
Qy 590 GAAGCTTTTACGTTTCAGCCCGGAGAACTCCATATCTGCGGGCACCTTTTTCGAGCGAGGGA 649
Db 607 TGCCGCTCCAGAACCTCAGCCCTCCCGTTCGCCGCGAGACCACTGGCTGTGCACAGAGA 666
Qy 650 ATTGGCAGAGCGAAATAGTCGAAAGATTTACGGAACCTACCGTTATGTTGTACAGTTGG 709
Db 667 GCTGGCCCAACCAACGCAACCGTCTGGCCTACACGACCTCCCTGCTGCTCTTCCAGTACT 726
Qy 710 TCGTGGCGATGGCAGTGATCAGTATTCCTACTTCAAAATCTTGC 754
Db 727 TCCTGCCCGCTGGGCTGATCGCGCTCTACTTGAAGCATCTTCC 771

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Search completed: May 8, 2006, 16:33:18  
Job time : 6325 secs



GenCore version 5.1.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2006, 14:28:24 ; Search time 5402 Seconds  
(without alignments)  
10332.653 Million cell updates/sec

Title: US-10-650-467-104  
Perfect score: 1193  
Sequence: 1 atggttagttcggggccac.....tgtcaggcaactttttcta 1193

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hic:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gses1:\*  
10: gb\_gses2:\*  
11: gb\_gses3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	684	57.3	801	7	CV124545 OSTF30030
2	579	48.5	615	3	BJ113336 BJ113336
3	509	42.7	543	3	BJ759866 BJ759866
4	471	39.5	749	3	BJ142720 BJ142720
5	435	36.5	469	3	BJ762291 BJ762291
6	360.4	30.2	366	3	BJ117135 BJ117135
7	297	24.9	713	3	BJ786750 BJ786750
8	257	21.5	258	3	BJ767176 BJ767176
9	153.4	12.9	530	3	BI451132 kx11b03.y
10	102.4	8.6	477	3	BJ784215 BJ784215
11	100	8.4	445	3	BJ153679 BJ153679
12	85.6	7.2	608	10	CZ209081
13	84	7.0	578	6	CB402398 OSTF212A4
14	80	6.7	850	1	AI438264 SMOVAFCAP
15	79.6	6.7	537	6	CB402411 OSTF212C1
16	70.2	5.9	616	3	BJ763929 BJ763929
17	66.6	5.6	575	1	AUI98665 AUI98665
18	66	5.5	794	8	CK796754 JGI_CAAJ1
19	64.8	5.4	792	5	BU218881 603756577
20	64.8	5.4	813	5	BU363760 603787987
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22	62.8	5.3	820	6	CA939929 ru75a09.y

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24	60.2	5.0	276	3	BJ144795
25	58.4	4.9	594	3	BP228990
26	58.2	4.9	777	5	BU489814
27	57.8	4.8	591	7	CV024564
28	57.8	4.8	718	7	CO959636
29	57.8	4.8	1152	10	AY413581
30	57.8	4.8	1155	10	AY413580
31	57.6	4.8	1168	10	AY409053
32	57.2	4.8	875	5	BX617017
33	56.8	4.8	803	6	CD559637
34	56.6	4.7	515	2	BF286067
35	56.2	4.7	455	6	CB741495
36	56	4.7	550	3	BJ108410
37	56	4.7	564	5	BJ738447
38	55.2	4.6	660	8	DR983057
39	55.2	4.6	706	8	DR982513
40	55.2	4.6	718	8	DR985305
41	55.2	4.6	718	8	DR985306
42	55.2	4.6	728	8	DR982514
43	55.2	4.6	737	8	DR983058
44	55.2	4.6	795	6	CD559636
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## ALIGNMENTS

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LOCUS  
DEFINITION OSTF30030H01 pDONR201 Entry vector Caenorhabditis elegans cDNA, linear EST 31-AUG-2004  
ACCESSION CV124545  
VERSION CV124545.1 GI:51715739  
KEYWORDS EST.  
SOURCE Caenorhabditis elegans  
ORGANISM Caenorhabditis elegans  
REFERENCE 1 (bases 1 to 801)  
AUTHORS Lamesch,P., Milstein,S., Hao,T., Rosenberg,J., Li,N., Sequerra,R., Bosak,S., Doucette-Stamm,L., Vandenhaute,J., Hill,D.E. and Vidal,M.  
TITLE C. elegans Orfome Version 3.1: Increasing the coverage of Orfome resources with improved gene predictions  
JOURNAL Genome Res. (Orfome issue) (2004) In press  
COMMENT Contact: Philippe Lamesch and Tong Hao  
Marc Vidal Lab  
DFCI  
44, Binney Street, Boston, MA 02115, USA  
Tel: 6176323910  
Fax: 6176325739  
Email: philippe\_lamesch@dfci.harvard.edu  
PCR Primers  
FORWARD: TGGTAGTTGGCGGCCACCAT  
BACKWARD: TAGAAGAGTTCCTGCACAT.  
Location/Qualifiers  
1. 801  
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Best Local Similarity 98.3%; Pred. No. 1e-191;

Matches 702; Conservative 0; Mismatches 10; Indels 2; Gaps 1;

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QY 182 TCTACGGGTTCTGTTGTTATGAGCAATTTTGAAGCGGCGGTACTATGGCGGGTGG 241
Db 181 TCTACGGGTTCTGTTGTTATGAGCAATTTTGAAGCGGCGGTACTATGGCGGGTGG 240
QY 242 CGAGAAACAAGCGGCTCCAAATCGGCTCGCAACGTAATTTCTGCTCAACTTGTATCTTCACCG 301
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Db 361 GGGCAATTCGGGTCAGTGATGCGCAATTTAGTTCCTTCTGTCCTCAATTCGGTTCGGTGGTTG 420
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QY 602 TTCAGCCGGAGAAACTCCATCTACCTCGGCGCACTTTTGGACAGAGCGAAATGGCAGAGCG 661
Db 601 TTCAGCCGGAGAAACTCCATCTACCTCGGCGCACTTTTGGACAGAGCGAAATGGCAGAGCG 660
QY 662 AAAATAGTCGAAAGATTTACGAA--CTACGGTTATGTTGTTACAGTTCGTCGT 713
Db 661 AAAATAGTCGAAAGATTTACGGAAGCTACCGTTATGTTGTTAAACAGTTTCGT 714
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BJ113336 615 bp mRNA linear EST 23-JAN-2002
LOCUS BJ113336 unpublished oligo-capped cDNA library, C. elegans L1 stage
DEFINITION Caenorhabditis elegans cDNA clone yk1166h04 5', mRNA sequence.
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ACCESSION BJ113336
VERSION BJ113336.1 GI:18273407
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditicoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
AUTHORS and Sugano, S.
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2002)
COMMENT Contact: Tadao Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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Matches 579; Conservative 0; Mismatches 1;
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QY 421 GTGACGAGTTGGAGCTCACTGCAATCTCTTATGCTTTTCGAGC 580
Db 456 GTGACGAGTTGGAGCTCACTGCAATCTCTTATGCTTTTCGAGC 615
QY 481 ACCAACAACAGGTTCTTATTCGTCAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540
Db 516 ACCAACAACAGGTTCTTATTCGTCAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 575
QY 541 TCAACACTGATAAATCTACCGTATCTTATGCTTTTCGAGC 580
Db 576 TCAACACTGATAAATCTACCGTATCTTATGCTTTTCGAGC 615
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LOCUS BJ113336 unpublished oligo-capped cDNA library Caenorhabditis
DEFINITION elegans cDNA clone yk1532c11 5', mRNA sequence.
ACCESSION BJ113336
VERSION BJ113336.1 GI:47599628
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditicoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
AUTHORS 1 (bases 1 to 543)
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SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Caenorhabditis elegans  
Caenorhabditis elegans  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.  
1 (bases 1 to 713)  
Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.  
and Sugano,S.  
A complementary view of the C.elegans genome  
Unpublished (2002)  
Contact: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp.

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Db 653 GGTGTGCATTTATTCGGGTGTGGTTCCTTTAATTTGCTCAATTTGGTCAAGATTT 594  
QY 933 TAAAAAGAGCCGGAATGCTAAAAAGTCAAGCGTCTTCTGGGCAATAAATGCTCAGT 992  
Db 593 TAAAAAGAGCCGGAATGCTAAAAAGTCAAGCGTCTTCTGGGCAATAAATGCTCAGT 534  
QY 993 CATAGCCATGCTTTAGTGTGCTGGAACCCCTCTGCTATTCTTTTGGCTGACACGAAACA 1052  
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QY 1053 AAAAGTTCCGGACTGTCAAAATACTCAACTCAACAG----- 1090  
Db 473 AAAAGTTCCGGACTGTCAAAATACTCAACTCAACAGAGATTGTCTCTGTTGCCAG 414  
QY 1091 -----ACGGTTCG 1098  
Db 413 TAGAGTGAATTAATCGATTCGGCGTCAACGTTTCGGAGAAACAATATTGACAGGGTTCG 354  
QY 1099 AAAAAGCAGGTGGTCTTGATTCGAGGGATCCAGCTACAGACCTCTCCCGACCTCT 1158  
Db 353 AAAAAGCAGGTGGTCTTGATTCGAGGGATCCAGCTACAGACCTCTCCCGACCTCT 294  
QY 1159 ACTCATTCGGACAGATGTGCGGCAACTCTTTCTTA 1193  
Db 293 ACTCATTCGGACAGATGTGCGGCAACTCTTTCTA 259

RESULT 8  
LOCUS  
DEFINITION  
AUTHORS  
ACCESSION  
VERSION

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BJ767176 unpublished oligo-capped cDNA library  
Caenorhabditis  
elegans cDNA clone yk1655f07 5', mRNA sequence.  
BJ767176  
BJ767176.1 GI:47630881

EST.  
Caenorhabditis elegans  
Caenorhabditis elegans  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.  
1 (bases 1 to 258)  
Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.  
and Sugano,S.  
A complementary view of the C.elegans genome  
Unpublished (2002)  
Contact: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp.

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Best Local Similarity 99.6%; Pred. No. 8.8e-65;  
Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 124 GCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTC 183  
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QY 184 TACGGTTCCTGTTGTATTAGGCATTTTGGAAACGGCGGCTACTATGCGGGTGGG 243  
Db 121 TACGGTTCCTGTTGTATTAGGCATTTTGGAAACGGCGGCTACTATGCGGGTGGG 180  
QY 244 AGAAACAAGCGCTCCAATCGCTCGCAACGTTATTCGCTCAACTTGATCTTCACCGAT 303  
Db 181 AGAAACAAGCGCTCCAATCGCTCGCAACGTTATTCGCTCAACTTGATCTTCACCGAT 240  
QY 304 TTGATATTGGTGTTCACA 321  
Db 241 TTGATATTGGTGTTCACA 258

RESULT 9  
LOCUS  
DEFINITION  
AUTHORS  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

BI451132  
kx11b03.v3 Parastrongyloides trichosuri IL PAMP1 v1 Chiapelli  
McCarte Parastrongyloides trichosuri cDNA 5' similar to WP:CE24480  
Y58G8A.3 seven trans-membrane receptor i, mRNA sequence.  
BI451132  
BI451132.1 GI:15275839  
EST.  
Parastrongyloides trichosuri  
Parastrongyloides trichosuri  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
Panagrolaimoidea; Strongyloidea; Parastrongyloidea.  
1 (bases 1 to 530)  
McCarte,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,  
Wyllie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,  
Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,

Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,  
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
McCann, R., Waterston, R., and Wilson, R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)  
Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
The library was constructed by Brandi Chiapelli and Dr. James  
McCarter (bchiapelle@wustl.edu & jmcarter@wustl.edu) at  
Washington University, St. Louis. DNA Sequencing by: Washington  
University Genome Sequencing Center St. Louis.  
High quality sequence stop: 384.  
Location/Qualifiers  
FEATURES  
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Chiapelli McCarter"  
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The library was constructed by Brandi Chiapelli and Dr.  
James McCarter at Washington University, St. Louis. The  
cDNA was made by using Dynabead oligo-dT priming (Dynal).  
PCR based library using a modified protocol from the  
SMART PCR cDNA Synthesis Kit from Clontech. Directionally  
cloned into the UDG sites of pAMP1. Nematodes were  
provided by Dr. Warwick Grant of AgResearch, New Zealand  
(warwick.grant@agresearch.co.nz)."

## ORIGIN

Query Match 12.9%; Score 153.4; DB 3; Length 530;  
Best Local Similarity 57.5%; Pred. No. 7.3e-34;  
Matches 296; Conservative 0; Mismatches 216; Indels 3; Gaps 1;  
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QY 469 ATCAACGATCCCAACCAACCAACAGTTCCTATTCCTCAAGCGTTGGCAATTAACATTTCT 528  
DB 71 ATTGTAAATCCTATTAGGCAACCAAGTATCAATAAATCAAGCAATATATAACAAATTTCT 130  
QY 529 ATCTGGATAGTCTCAACAGTAAATCTACCGTATCTTATGTCTTTTCGAGCAGCTCGAT 588  
DB 131 ATATGGATATATCAATTTCTAGCAATATATCCACCTATTTGTTAAATTTCTGATCTCAAAATCG 190  
QY 589 GGA---AGCTTTTACGTTTCAGCCCGGAGAAATCCCATCTCGCGGCACTTTTGGCAGCAG 645  
DB 191 GGAGATGCTTTTACAGTTTCATTGAGATAAAACCAATATGTCGAGTTTGTGTA 250  
QY 646 GCGAATTTGGCAGAGGAAATATAGTCGAAAGATTTACGGAATCTACCGTATGTTGTACAG 705  
DB 251 GAGACATGGGAAATATGTCGAGCAGACAAAGTATGATTAATGTCATTAATTTTCCAA 310  
QY 706 TTCGTCGTCGAGTCAGTATGTCAGTATGTCATCTCAAAATCTTGCAGCAAGTCA 765  
DB 311 TTTTATTTGACCAATGGAATAATAACATATTTTACTGGAGAAATTTCTCATAAGTTGCT 370  
QY 766 AAGACATGATCATCAAAATGCTCAATTTCTGTCATCTGACACACAAAGCAGAGAACT 825  
DB 371 AAGATTTCAATTAATTCACATGTTTCAATTTTCAATTTTCAATTTTATCAGCATCAACGAAT 430  
QY 826 GATCGACGTCACGAAAGAAAGTGAATTAATTTCTAATTTGCAATGTTGTCAATTT 885  
DB 431 GCTGCTATCAATAGAAAGAGACGAGTAATTAATTTAATTTGCAATGTTGTGCTTTT 490

QY 886 ATCGGGTGTGTTGCTTCTTAACTACTCAATTT 920  
DB 491 ATATTATGTTGGTTTCGTTTACAAATTTATATAT 525  
RESULT 10  
BJ784215/c  
LOCUS  
DEFINITION  
BJ784215 unpublished oligo-capped cDNA library Caenorhabditis  
elegans cDNA clone yk1532c11 3', mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Caenorhabditis elegans  
Caenorhabditis elegans  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
Rhabditoidea; Rhabditidae; Pelodierinae; Caenorhabditis.  
REFERENCE  
1 (bases 1 to 477)  
Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.  
and Sugano, S.  
A complementary view of the C.elegans genome  
Unpublished (2002)  
Contact: Tadaasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp.  
Location/Qualifiers  
FEATURES  
source  
1..477  
/organism="Caenorhabditis elegans"  
/mol\_type="mRNA"  
/strain="N2"  
/db\_xref="taxon:6239"  
/clone="yk1532c11"  
/sex="Hermaphrodite"  
/tissue\_type="whole animal"  
/dev\_stage="varied"  
/clone\_lib="unpublished oligo-capped cDNA library"  
ORIGIN  
Query Match 8.6%; Score 102.4; DB 3; Length 477;  
Best Local Similarity 98.1%; Pred. No. 1.1e-18;  
Matches 103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1089 AGAGGTTTCGAAAAAAGCAGGTGTTCTGGATTGGAGGATCCAGCTACGACCTCT 1148  
DB 359 ACAGGTTTCGAAAAAAGCAGGTGTTCTGGATTGGAGGATCCAGCTACGACCTCT 300  
QY 1149 CCGGACCTCTACTCATTCGGACAGATGTCAGGCAACTCTTTCTA 1193  
DB 299 CCGGACCTCTACTCATTCGGACAGATGTCAGGCAACTCTTTCTA 255  
RESULT 11  
BJ153679/c  
LOCUS  
DEFINITION  
BJ153679 unpublished oligo-capped cDNA library, C. elegans L1 stage  
Caenorhabditis elegans cDNA clone yk1322b09 3', mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Caenorhabditis elegans  
Caenorhabditis elegans  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
Rhabditoidea; Rhabditidae; Pelodierinae; Caenorhabditis.  
REFERENCE  
1 (bases 1 to 445)  
Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.  
and Sugano, S.  
A complementary view of the C.elegans genome  
Unpublished (2002)  
Contact: Tadaasu Shin-i



Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp.

#### FEATURES

source

1. .445  
Location/Qualifiers  
/organism="Caenorhabditis elegans"  
/mol\_type="mRNA"  
/strain="N2"  
/db\_xref="taxon:6239"  
/clone="yk1322b09"  
/sex="hermaphrodite"  
/tissue\_type="whole animal"  
/dev\_stage="L1"  
/clone\_lib="unpublished oligo-capped cDNA library, C. elegans L1 stage"

#### ORIGIN

Query Match 8.4%; Score 100; DB 3; Length 445;  
Best Local Similarity 97.1%; Pred. No. 5.4e-18;  
Matches 100; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1091 AGGGTTGGAAGGAGGCTGCTCTGGATTGCGAGGATCCAGCTACAGACCTCTCC 1150  
DB 373 AGGGTTGGAAGGAGGCTGCTCTGGATTGCGAGGATCCAGCTACAGACCTCTCC 314  
QY 1151 CGACCTTACTCATTGCGACAGATGTCAGGCACTCTTTCTA 1193  
DB 313 CGACCTTACTCATTGCGACAGATGTCAGGCACTCTTTCTA 271

#### RESULT 12

CZ209081/c  
LOCUS 608 bp DNA linear GSS 10-PEB-2005  
DEFINITION A1AA-aad9110.g1 Ancylostoma caninum whole genome shotgun library (A1AAGSS 001) Ancylostoma caninum genomic, genomic survey sequence.  
ACCESSION CZ209081  
VERSION CZ209081.1 GI:59212954  
KEYWORDS GSS.  
SOURCE Ancylostoma caninum (dog hookworm)  
ORGANISM Ancylostoma caninum  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.  
1 (bases 1 to 608)  
Ronko, I., Martin, J., Wylie, T., Dante, M., Meyer, R., Messina, D., Waterston, R.H., Clifton, S.W. and Wilson, R.  
Genome Survey sequences from the parasitic nematode Ancylostoma caninum  
Unpublished (2004)  
Contact: Mitreva M  
Washington University in St. Louis  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: nematode@watson.wustl.edu  
Genomic DNA provided by John Hawdon (mtmjhg@wumc.edu) DNA sequenced by Washington University Genome Sequencing Center  
Class: shotgun.

#### FEATURES

source

Location/Qualifiers  
1. .608  
/organism="Ancylostoma caninum"  
/mol\_type="genomic DNA"  
/strain="Baltimore"  
/db\_xref="taxon:29170"  
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/lab\_host="GS10"  
/clone\_lib="Ancylostoma caninum whole genome shotgun library (A1AAGSS 001)"  
/note="Vector: pOTW13; Site\_1: BstX1; Site\_2: BstX1;

Ancylostoma caninum genomic DNA was randomly sheared, end-repaired and size fractionated to enrich for 2-4 kb fragments. Genomic DNA was provided by John Hawdon (mtmjhg@wumc.edu) at George Washington University. Sequencing by Washington University Genome Sequencing Center, St. Louis, MO."

#### ORIGIN

Query Match 7.2%; Score 85.6; DB 10; Length 608;  
Best Local Similarity 64.8%; Pred. No. 1.1e-13;  
Matches 127; Conservative 0; Mismatches 69; Indels 0; Gaps 0;  
QY 152 ACTTTTACATCGATCAATCTTCACATTCCTCAGGGTTCCTGTTGTTATAGGCATTT 211  
DB 319 AATTGTTCTCAAAATCGGGTTACGGCTCTCTACGGCTTTCTGTTTCATCTCTG 260  
QY 212 TTGGAACCGCGCGCTACTATGCGGGTGGCGAGAAACAAAGCGGCTCCAAATCGGCTCGCA 271  
DB 259 TCGGCAATGGTGGCGTGTATTTGCAATGGCGAATAATCGCGACTACGGTCAGCAGGA 200  
QY 272 AGTATTTCTGCTCAACTTGATCTTCACGATTTGATATTTGGTGTTCACAGGATTCAG 331  
DB 199 ACATATTTCTGCTCAATCTGATCTACTGATCTGCTACTTGTACTCACTGCGGTACCTG 140  
QY 332 TCACACCATGGTACGC 347  
DB 139 TTACGCTTGGTAGGC 124

#### RESULT 13

CZ209081/c  
LOCUS 578 bp mRNA linear EST 15-MAY-2003  
DEFINITION OSTF212A4\_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.  
ACCESSION CB402398  
VERSION CB402398.1 GI:30744125  
KEYWORDS EST.  
SOURCE Caenorhabditis elegans  
ORGANISM Caenorhabditis elegans  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.  
1 (bases 1 to 578)  
Reboul, J., Vaglio, P., Rual, J.P., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.B., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.  
C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression  
Nat. Genet. (2003) In press  
Contact: Vidal M  
Marc Vidal Laboratory  
Dana Farber Cancer Institute  
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
Tel: 617 632 5180  
Fax: 617 632 5739  
Email: Marc.Vidal@dfci.harvard.edu  
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david\_hill@dfci.harvard.edu or marc\_vidal@dfci.harvard.edu  
POLYA=No.

#### JOURNAL COMMENT

#### FEATURES

Location/Qualifiers  
1. .578  
/organism="Caenorhabditis elegans"  
/mol\_type="mRNA"  
/strain="N2"  
/db\_xref="taxon:6239"  
/sex="Hermaphrodite and male"  
/tissue\_type="whole animal"  
/dev\_stage="mixed stage"  
/clone\_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

ORIGIN	
Query Match	7.0%; Score 84; DB 6; Length 578;
Best Local Similarity	50.5%; Pred. No. 3.3e-13;
Matches	204; Conservative 0; Mismatches 200; Indels 0; Gaps 0;
Qy	167 CAATCTTCAATCTCTACGGGTCCTGTTGATTTAGGCAATTTTGGAAACGGCGGCG 226
Db	85 CGATTCTTGCACCACTACACTATAATTGCTAGTTGGCGTAACCGGCAATTTGTTAG 144
Qy	227 TACTATCGGGGTCGCGAGAAACAGCGCTCCCAATCGGCTCGCAACGATATTTCTGCTCA 286
Db	145 TAGTGATGTCGGTGATGAGGTTCAAGTTCATCATGTCAGGACAGTTCATCGTAT 204
Qy	287 ACTTGATCTTCCACCGATTTGATATTTGGTGTTCACAGCGAATTCAGTCACACCATGGTACG 346
Db	205 CTTTGTGAGTTCTGACATTTTGTGGCGATTGTTAGTGTTCAGTAACGCGGATAACCG 264
Qy	347 CGATGACAAAGACTGGGCATTCGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAATTT 406
Db	265 CATTTCTCAAAAGTTGGTATTTTGGTGACCAATTTGTGTCATTTACTACCTTTGTACAGG 324
Qy	407 CGTGTTCGGTGTGTGACGAGTTGGAGCCTTCACCTGCAATCTCCTTAGATAAAATTTCTGC 466
Db	325 GTACGGGTTGAGTTTTCAGGTTTAAAGCTCAGTCACCGAATTCAGATGATATATTC 384
Qy	467 ATATCAACGATCCCAACCAACACAGTTTCTATTCGTCAAGCGGTGGCAATAACATTC 526
Db	385 TCATCTGTCTATCCGAGGAAGACCGATACGCAAGATCAAGCATTTGAAATGATAAGTT 444
Qy	527 TTATCTGATAGTCTCAACACTGATTAATCTACCGTATCTTATG 570
Db	445 TCAACAGCGCCATCTCTAGTTGGGCTTTTCGGTACCATTTATTCATG 488

RESULT 14  
A1438264  
LOCUS  
DEFINITION  
SWOVAFCAP29C10SK Onchocerca volvulus adult female cDNA  
(SAW98MLM-OvAF) Onchocerca volvulus cDNA clone SWOVAFCAP29C10 5',  
mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
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1. .850  
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/mol\_type="mRNA"  
/db\_xref="taxon:6282"  
/clone="SWOVAFCAP29C10"  
/sex="female"

/dev stage="adult"  
/lab\_host="Xli-Blue MRF"  
/Clone lib="Onchocerca volvulus adult female cDNA  
(SAW98MLM-OvAF)"  
/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:  
Xho I; Filarial nematode parasite of humans. Two adult  
female worms of Onchocerca volvulus were isolated from  
consenting patients and quick frozen. Adult female mRNA  
was converted to double-stranded cDNA using reverse  
transcriptase and oligo(dT) followed by RNase H and DNA  
pol I. The library has 7 x 10<sup>5</sup> independent recombinants  
and the average insert size is ~1100bp. The library was  
constructed by Michelle Lizotte-Waniewski with worms  
provided by Dr. Sara Lustigman. The library is available  
from Dr. Steven A. Williams, email: genome@smith.edu."

ORIGIN	
Query Match	6.7%; Score 80; DB 1; Length 850;
Best Local Similarity	50.2%; Pred. No. 5.8e-13;
Matches	205; Conservative 0; Mismatches 202; Indels 1; Gaps 1;
Qy	139 GATATTACTGTAGACTTTTACATCCGATCAATCTTCATCTCTACGGGTTCTGTTT 198
Db	167 GATTGGAGTACTCAGTCACTCTACCGTATTCATCTTCGTTTTTTTTTACGGAGCANTTATC 226
Qy	199 GTATTAGGCAATTTTGGAAACGGCGGTACTATGGCGGTGGGAGAAACAAGCGGCTC 258
Db	227 CTGATCGGTTAGTGGGCAACCTGTGCGTCATATCTGGCCATATCTAGGACCAGGACATG 286
Qy	259 CAATCGGCTGCCAACGATTTCTGCTCAACTTGTATCTTCACCGATTTGATATTTGTTTC 318
Db	287 CAAACAATACCAATNTGTTCAATTTTTTGTGAGCTGTTCCGAGCTGTTGTATGTTTT 346
Qy	319 ACAGCGATTCAGTCACACCAATGTTAGCGGATGACCAAGACTCGGGCAATTCGGGTCACTG 378
Db	347 ACTTCAGCGCAATNAGCGCGNTCAGGCGNTTCAAAAAGAGATGATCTTCGGTCTCTGA 406
Qy	379 ATGTGCCAATTTAGTTCCTTTGTCAATTCGTTGTTGGTGTGTTGACAGTTGGAGCTTC 438
Db	407 CTCTGCTCGATAGCTCCGTTTATTTGCTGGCACTTCACTGCTTCTCACAGTTTACTCTC 466
Qy	439 ACTGCAATCTCTTAGATAAAATTTCTGCATATCAACGATCCACCAACCAACAGTTTCT 498
Db	467 TCAGCAATCTCAGTGATCGTTTGTTCATCTATTTTCCGACTAGAAAGCTCTTTCC 526
Qy	499 ATTGCTC-AAGCGTTGGCAATAAATTTCTTATCTGATAGTCTCAAC 545
Db	527 AGGCTTCAAAGCAATNTTTCGTAATATGTTGTTNTGTCATATTTATCCAC 574

RESULT 15  
CB402411  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CB402411  
OSTP212C1\_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.  
CB402411  
CB402411.1 GI:30744138  
EST.  
Caenorhabditis elegans  
Caenorhabditis elegans  
Caenorhabditis elegans  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.  
1 (bases 1 to 537)  
Reboul,J., Vaglio,P., Rual,J.P., Lamesch,P., Martinez,M.,  
Armstrong,C.M., Li,S., Jacotot,L., Bortin,N., Janky,R., Moore,T.,  
Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,  
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,  
Tollas,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,  
Doucette-Stamm,L., Hill,D.E. and Vidal,M.  
C. elegans ORFome version 1.1: experimental verification of the  
genome annotation and resource for proteome-scale protein  
expression  
Nat. Genet. (2003) In press  
Contact: Vidal M



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GenCore version 5.1.8  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.  
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 (without alignments)  
 9803.919 Million cell updates/sec  
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 Perfect score: 1193  
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 Gapop 10.0 , Gapext 1.0  
 Searched: 4996997 seqs, 3332346308 residues  
 Total number of hits satisfying chosen parameters: 9993994  
 Minimum DB seq length: 0  
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 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

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 1: Geneseq1980s.\*  
 2: Geneseq1990s.\*  
 3: Geneseq2000s.\*  
 4: Geneseq2001as.\*  
 5: Geneseq2001bs.\*  
 6: Geneseq2002as.\*  
 7: Geneseq2002bs.\*  
 8: Geneseq2003as.\*  
 9: Geneseq2003bs.\*  
 10: Geneseq2003cs.\*  
 11: Geneseq2003ds.\*  
 12: Geneseq2004as.\*  
 13: Geneseq2004bs.\*  
 14: Geneseq2005s.\*  
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1193	100.0	1193	4 AAS07253	Aas07253 G protein
2	1193	100.0	1500	4 AAS07219	Aas07219 G protein
3	1109	93.0	1301	4 AAS07254	Aas07254 G protein
4	96.6	8.1	1130	4 AAS07210	Aas07210 G protein
5	84	7.0	1098	4 AAS07217	Aas07217 G protein
6	78.8	6.6	1352	4 AAS07208	Aas07208 G protein
7	66.6	5.6	1374	4 AAS07212	Aas07212 G protein
8	62.2	5.2	1965	2 AAS07212	Aas07212 G protein
9	62.2	5.2	2018	10 AAS07212	Aas07212 G protein
10	61.6	5.2	1302	3 AAS07212	Aas07212 G protein
11	61.6	5.2	1302	12 AAS07212	Aas07212 G protein
12	61.6	5.2	1302	14 AAS07212	Aas07212 G protein
13	61.6	5.2	1302	14 AAS07212	Aas07212 G protein
14	61.6	5.2	1440	3 AAS07212	Aas07212 G protein
15	61.6	5.2	1560	10 AAS07212	Aas07212 G protein
16	61.6	5.2	1560	10 AAS07212	Aas07212 G protein
17	61.6	5.2	1569	12 AAS07212	Aas07212 G protein
18	61.6	5.2	1569	12 AAS07212	Aas07212 G protein
19	61.6	5.2	1790	5 AAS07212	Aas07212 G protein

20	61.6	5.2	1824	4 ABA08967	Aba08967 Human GPC
21	61.6	5.2	1888	2 AAV68484	Aav68484 Human 7-t
22	61.6	5.2	1888	3 AAA61230	Aaa61230 DNA encod
23	61.6	5.2	1888	6 ABK47410	Abk47410 Human cDN
24	61.6	5.2	1903	3 AAZ86955	Aaz86955 Human cDN
25	61.6	5.2	1903	14 ADY84708	Ady84708 Human neu
26	61.6	5.2	1936	8 ABZ42862	Abz42862 Human neu
27	61.6	5.2	1936	10 ADC89683	Adc89683 Human neu
28	61.6	5.2	1936	10 ADE85182	Adh85182 Farnesyl
29	61.6	5.2	1936	12 ADH61950	Adh61950 Human neu
30	61.6	5.2	1936	12 ADQ21327	Adq21327 Human sof
31	61.6	5.2	1936	13 ADQ89055	Adq89055 Human uro
32	61.6	5.2	1938	12 ADQ25198	Adq25198 Human sof
33	60.2	5.0	1557	5 AAH49408	Aah49408 D. melano
34	60.2	5.0	1803	5 AAS05844	Aas05844 Fruit fly
35	60.2	5.0	1803	9 AAD57459	Aad57459 Fruit fly
36	60.2	5.0	1803	10 ADE14523	Adel4523 DNA encod
37	60.2	5.0	1803	11 ADL83601	Adl83601 Drosophil
38	60.2	5.0	1803	12 ADR03091	Adr03091 Drosophil
39	60.2	5.0	1803	14 ADV91971	Adv91971 DmGPCR1 c
40	60.2	5.0	2504	4 ABL29487	Ab129487 Drosophil
41	60.2	5.0	16870	4 ABL29486	Ab129486 Drosophil
42	60	5.0	1934	5 AAS00316	Aas00316 Orphan re
43	58.4	4.9	2708	2 AAV69220	Aav69220 Human G-p
44	57.8	4.8	1155	10 AAD62456	Aad62456 Human neu
45	57.8	4.8	1155	10 ADH53331	Adh53331 Human neu

## ALIGNMENTS

RESULT 1  
 AAS07253  
 ID AAS07253 standard; DNA; 1193 BP.  
 XX  
 AC AAS07253;  
 XX  
 DT 12-SEP-2001 (first entry)  
 XX  
 DE G protein-coupled receptor-like (GPCR-like) receptor DNA #23.  
 XX  
 KW G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;  
 KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;  
 KW neuromuscular disorder; human; nematode; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200138533-A2.  
 XX  
 PD 31-MAY-2001.  
 XX  
 PF 24-NOV-2000; 2000WO-US032225.  
 XX  
 PR 24-NOV-1999; 99US-0167523P.  
 XX  
 PA (PHAA ) PHARMACIA & UPJOHN.  
 XX  
 PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;  
 DR WPI; 2001-343952/36.  
 DR P-PSDB; AAU03851.  
 XX  
 PT Using G-protein-coupled receptor (GPCR)-like receptors to identify  
 PT candidate compounds for the treatment and prevention of invertebrate  
 PT parasites, especially helminths and insects.  
 XX  
 PS Claim 1; Page 173-175; 219pp; English.  
 XX  
 CC The sequence represents a DNA encoding a G protein-coupled receptor-like  
 CC (GPCR-like) receptor protein. GPCR-like receptors and their associated  
 CC nucleic acids may be used to identify candidate compounds for their  
 CC ability to modulate the activity of GPCRs. The sequences therefore are  
 CC useful for treating and preventing infection by endoparasitic and

CC ectoparasitic invertebrate parasites, especially helminths and insects,  
CC and particularly ailments related to aberrant neurological and  
CC neuromuscular function  
XX  
SQ Sequence 1193 BP; 326 A; 281 C; 256 G; 330 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1193; DB 4; Length 1193;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGGTTAGTTCGGGGCCACCAATTTGACACCAATTTCAACACCAAGACATCCCTCCACCATC 60  
Db 1 ATGGTTAGTTCGGGGCCACCAATTTGACACCAATTTCAACACCAAGACATCCCTCCACCATC 60  
Qy 61 AGCAAGCTTATCACAAGTCAATTCGAACCAATGGCTGTCATTCAGATCGCTGAGGCGATT 120  
Db 61 AGCAAGCTTATCACAAGTCAATTCGAACCAATGGCTGTCATTCAGATCGCTGAGGCGATT 120  
Qy 121 GCGGCACAAGGCATCGATGATTAATCTAGACTTTTACATCCGATCAATCTTCACATTC 180  
Db 121 GCGGCACAAGGCATCGATGATTAATCTAGACTTTTACATCCGATCAATCTTCACATTC 180  
Qy 181 CTCTACGGGTTCTGTTTGTATAGGCAATTTTGGAAACGGGGCGTACTATGGCGGTG 240  
Db 181 CTCTACGGGTTCTGTTTGTATAGGCAATTTTGGAAACGGGGCGTACTATGGCGGTG 240  
Qy 241 GCGGAAACAAGCGGCTCAATCGGCTCGAACGTAATTTCTGCTCAACTTGATCTTCACC 300  
Db 241 GCGGAAACAAGCGGCTCAATCGGCTCGAACGTAATTTCTGCTCAACTTGATCTTCACC 300  
Qy 301 GATTTGATTTGGTGTTCACAGCGGATCCAGTCAACACCATGTCAGCGATGACCAAGAC 360  
Db 301 GATTTGATTTGGTGTTCACAGCGGATCCAGTCAACACCATGTCAGCGATGACCAAGAC 360  
Qy 361 TGGGCATTCCGGTCAAGTGTGATGATTCATTTAGTCTCTTTGTCAAATTCGTGTGGTGT 420  
Db 361 TGGGCATTCCGGTCAAGTGTGATGATTCATTTAGTCTCTTTGTCAAATTCGTGTGGTGT 420  
Qy 421 GTGACGAGTTGGAGCTCACTGCAATCTCTTAGATAAATTTCTGCATATCAACGATCCC 480  
Db 421 GTGACGAGTTGGAGCTCACTGCAATCTCTTAGATAAATTTCTGCATATCAACGATCCC 480  
Qy 481 ACCAAACAACAGTTTCTATTGTCGAAGCTTGGCAATAACATTTCTTATCTGGATGTC 540  
Db 481 ACCAAACAACAGTTTCTATTGTCGAAGCTTGGCAATAACATTTCTTATCTGGATGTC 540  
Qy 541 TCAACACTGATAAATCTACCGTATCTTATGCTCTTTGAGCAGCTCGATGGAGCTTTTAC 600  
Db 541 TCAACACTGATAAATCTACCGTATCTTATGCTCTTTGAGCAGCTCGATGGAGCTTTTAC 600  
Qy 601 GTTCAGCCGGAGAACTCCATCTACTGCGGGCACTTTTGGAGCAGGCGAATTTGGCAGAGC 660  
Db 601 GTTCAGCCGGAGAACTCCATCTACTGCGGGCACTTTTGGAGCAGGCGAATTTGGCAGAGC 660  
Qy 661 GAAATAGTCGAAGATTTACGGAATCTAGGTTATGTTTACAGTCTGCTGTCGCGGATG 720  
Db 661 GAAATAGTCGAAGATTTACGGAATCTAGGTTATGTTTACAGTCTGCTGTCGCGGATG 720  
Qy 721 GCAGTGATCAGCTATTTGCTACTTCAAAATCTTGGAAAAAGTGTCAAAAAGACATGATC 780  
Db 721 GCAGTGATCAGCTATTTGCTACTTCAAAATCTTGGAAAAAGTGTCAAAAAGACATGATC 780  
Qy 781 CAAAATGCTCAATCTGTCATCTACGACCAAAAGCAGAGATGATGCGAGCTCAGCA 840  
Db 781 CAAAATGCTCAATCTGTCATCTACGACCAAAAGCAGAGATGATGCGAGCTCAGCA 840  
Qy 841 AAGAAAGTCAATTTATTTCTAATTCGAATGTTTGCATTTATCGGTTGTTGGTTG 900  
Db 841 AAGAAAGTCAATTTATTTCTAATTTGCAATTTGTTGTTGTTGTTGTTGTTGTTGTTG 900  
Qy 901 CTTTAAACATTAATCAATTTGGTCAAGATTTTAAAAAGAGCCCGGAATGGCTAAACGT 960  
Db 901 CTTTAAACATTAATCAATTTGGTCAAGATTTTAAAAAGAGCCCGGAATGGCTAAACGT 960

Qy 961 CAGCGTTCTTCTGGCAATAAATGCTCAGCTATAGCAATGCTCTTAGTCTGTTGGAAC 1020  
Db 961 CAGCGTTCTTCTGGCAATAAATGCTCAGCTATAGCAATGCTCTTAGTCTGTTGGAAC 1020  
Qy 1021 CCTCTGCTATTTCTTTTGGCTGACACGAAACAAACGTTCCGGACTGTCAAAATATCTC 1080  
Db 1021 CCTCTGCTATTTCTTTTGGCTGACACGAAACAAACGTTCCGGACTGTCAAAATATCTC 1080  
Qy 1081 AACTCAACAGAGGTTTGGAAAAAGAGAGGTTTCTGATTTGCGAGGATCCAGCTACAC 1140  
Db 1081 AACTCAACAGAGGTTTGGAAAAAGAGAGGTTTCTGATTTGCGAGGATCCAGCTACAC 1140  
Qy 1141 GACCTCTCCGACCTCTACTCATTCGACAGATGTCAGCAACTCTTTCTA 1193  
Db 1141 GACCTCTCCGACCTCTACTCATTCGACAGATGTCAGCAACTCTTTCTA 1193  
RESULT 2  
AAS07219  
ID AAS07219 standard; DNA; 1500 BP.  
XX  
XX AAS07219;  
XX  
XX 12-SEP-2001 (first entry)  
XX  
XX G protein-coupled receptor-like (GPCR-like) receptor DNA #19.  
XX  
XX G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;  
KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;  
KW neuromuscular disorder; human; nematode; ds.  
XX  
XX Homo sapiens.  
XX  
XX WO200138533-A2.  
XX  
XX 31-MAY-2001.  
XX  
XX 24-NOV-2000; 2000WO-US032225.  
XX  
XX 24-NOV-1999; 99US-0167523P.  
XX  
XX (PHAA ) PHARMACIA & UPJOHN.  
XX  
XX Lowery DE, Geary TG, Kubiak TM, Larsen MJ;  
XX  
XX WPI; 2001-343952/36.  
XX  
XX P-PSDB; AAU03820.  
XX  
XX Using G-protein-coupled receptor (GPCR)-like receptors to identify  
PT candidate compounds for the treatment and prevention of invertebrate  
PT parasites, especially helminths and insects.  
XX  
XX Claim 1; Page 145-147; 219pp; English.  
XX  
XX The sequence represents a DNA encoding a G protein-coupled receptor-like  
CC (GPCR-like) receptor protein. GPCR-like receptors and their associated  
CC nucleic acids may be used to identify candidate compounds for their  
CC ability to modulate the activity of GPCRs. The sequences therefore are  
CC useful for treating and preventing infection by endoparasitic and  
CC ectoparasitic invertebrate parasites, especially helminths and insects,  
CC and particularly ailments related to aberrant neurological and  
CC neuromuscular function  
XX  
XX Sequence 1500 BP; 426 A; 322 C; 291 G; 461 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 1193; DB 4; Length 1500;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGGTTAGTTCGGGGCCACCAATTTGACACCAATTTCAACACCAAGACATCCCTCCACCATC 60  
Db 307 ATGGTTAGTTCGGGGCCACCAATTTGACACCAATTTCAACACCAAGACATCCCTCCACCATC 366



QY 61 AGCAACGTTATCACAAGTCATTGCAACATGGCTCGTGCAATTCAGATCGCTGAGGCGATT 120  
DB |||||  
QY 367 AGCAACGTTATCACAAGTCATTGCAACATGGCTCGTGCAATTCAGATCGCTGAGGCGATT 426  
DB |||||  
QY 121 GCGGCACAAGGCATCGATGATATTTACTGTAGACTTTTATCATCCGATCAATCTTTCACATTC 180  
DB |||||  
QY 427 GCGGCACAAGGCATCGATGATATTTACTGTAGACTTTTATCATCCGATCAATCTTTCACATTC 486  
DB |||||  
QY 181 CTCTACGGGTTCTGTTTGTATTTAGGCAATTTTGGAAACGGCGCGTACTATGGGCGGTG 240  
DB |||||  
QY 487 CTCTACGGGTTCTGTTTGTATTTAGGCAATTTTGGAAACGGCGCGTACTATGGGCGGTG 546  
DB |||||  
QY 241 GCGAGAAACAAGCGGCTCCAAATCGGCTCGCAAGTATTTCTGCTCAACTTGATCTTCACC 300  
DB |||||  
QY 547 GCGAGAAACAAGCGGCTCCAAATCGGCTCGCAAGTATTTCTGCTCAACTTGATCTTCACC 606  
DB |||||  
QY 301 GATTTGATATTTGTTTCAAGGATTTCCAGTCACACCATGGTATCGCGATGACCAAGAC 360  
DB |||||  
QY 607 GATTTGATATTTGTTTCAAGGATTTCCAGTCACACCATGGTATCGCGATGACCAAGAC 666  
DB |||||  
QY 361 TGGGCATTCGGGTCAGTGATGCGCAATTTAGTTCCTTTGTCAAATTCGTTTCGGTGT 420  
DB |||||  
QY 667 TGGGCATTCGGGTCAGTGATGCGCAATTTAGTTCCTTTGTCAAATTCGTTTCGGTGT 726  
DB |||||  
QY 421 GTGACGAGTTGGAGCCTCACTGCAATCTCTTAGATAAATTTCTGCATATCAACGATCCC 480  
DB |||||  
QY 727 GTGACGAGTTGGAGCCTCACTGCAATCTCTTAGATAAATTTCTGCATATCAACGATCCC 786  
DB |||||  
QY 481 ACCAAACAACCAAGTTCTTCTATTCGTCAAGGTTGGCAATTAACATTTCTTATCTGGATGTC 540  
DB |||||  
QY 787 ACCAAACAACCAAGTTCTTCTATTCGTCAAGGTTGGCAATTAACATTTCTTATCTGGATGTC 846  
DB |||||  
QY 541 TCAACATGATAAATCTACCGTATCTTATGTCTTTTCGAGCAGTCGATGGAAGCTTTTAC 600  
DB |||||  
QY 847 TCAACATGATAAATCTACCGTATCTTATGTCTTTTCGAGCAGTCGATGGAAGCTTTTAC 906  
DB |||||  
QY 601 GTTCAGCCCGGAGAACTCATACTCGCGGCACTTTTGGACGAGCGGAATTTGGCAGAGC 660  
DB |||||  
QY 907 GTTCAGCCCGGAGAACTCATACTCGCGGCACTTTTGGCAGCAGCGGAATTTGGCAGAGC 966  
DB |||||  
QY 661 GAAATATGTCGAAAGATTTACGGAATACGGTTATGTTGTATACAGTTCTGTCGCGGATG 720  
DB |||||  
QY 967 GAAATATGTCGAAAGATTTACGGAATACGGTTATGTTGTATACAGTTCTGTCGCGGATG 1026  
DB |||||  
QY 721 CGAGTGATCAGTATTTGCTACTTCAAATCTTTGCAAAAAGTGTCAAAGACATGATCATC 780  
DB |||||  
QY 1027 CGAGTGATCAGTATTTGCTACTTCAAATCTTTGCAAAAAGTGTCAAAGACATGATCATC 1086  
DB |||||  
QY 781 GAAATGCTCAATTTCTGTCATCTGACACAAAAGCAGAGAAGTGATCGGACGTACGA 840  
DB |||||  
QY 1087 GAAATGCTCAATTTCTGTCATCTGACACAAAAGCAGAGAAGTGATCGGACGTACGA 1146  
DB |||||  
QY 841 AAGAAGAAGTCAATTTATATTTCTTAATGCAATGTTGTGCACATTTATCGGTTGGTTG 900  
DB |||||  
QY 1147 AAGAAGAAGTCAATTTATATTTCTTAATGCAATGTTGTGCACATTTATCGGTTGGTTG 1206  
DB |||||  
QY 901 CTTTAAACATTAATCAATTTGCTCAAGATTTTAAAAAGACCCGAATGGCTTAAACGT 960  
DB |||||  
QY 1207 CTTTAAACATTAATCAATTTGCTCAAGATTTTAAAAAGACCCGAATGGCTTAAACGT 1266  
DB |||||  
QY 961 GAGCGGTTCTTCTGGGCAATAAATGCTCAGTCATAGCCATGCTCTTAGTCTGTGGAAC 1020  
DB |||||  
QY 1267 GAGCGGTTCTTCTGGGCAATAAATGCTCAGTCATAGCCATGCTCTTAGTCTGTGGAAC 1326  
DB |||||  
QY 1021 CCTCTGCTATTTCTTTTGGCTGACAGAAACAAAACGTTCCGGACTGTCAAAATATCTC 1080  
DB |||||  
QY 1327 CCTCTGCTATTTCTTTTGGCTGACAGAAACAAAACGTTCCGGACTGTCAAAATATCTC 1386  
DB |||||  
QY 1081 AACTCAACAGAGGGTTTCAAAAAAAGCAGGTGTTCTGGAATTCGAGGAGATCCAGCTACAC 1140  
DB |||||  
QY 1387 AACTCAACAGAGGGTTTCAAAAAAAGCAGGTGTTCTGGAATTCGAGGAGATCCAGCTACAC 1446  
DB |||||

QY 1141 GACCTCCTCCCGACCTCTACTCTACTTCGAGACAGATGTCAGGCAACTCTTTCTA 1193  
DB |||||  
QY 1447 GACCTCCTCCCGACCTCTACTCTACTTCGAGACAGATGTCAGGCAACTCTTTCTA 1499  
DB |||||

## RESULT 3

AAS07254  
ID AAS07254 standard; DNA; 1301 BP.

XX AC AAS07254;  
XX DT 12-SEP-2001 (first entry)

XX G protein-coupled receptor-like (GPCR-like) receptor DNA #24.  
DE G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;  
XX endoparasite; ectoparasite; invertebrate; insect; neurological disorder;  
KW neuromuscular disorder; human; nematode; ds.  
XX OS Homo sapiens.

XX WO200138533-A2.

XX 31-MAY-2001.

XX 24-NOV-2000; 2000WO-US032225.

XX 24-NOV-1999; 99US-0167523P.

XX (PHAA ) PHARMACIA & UPJOHN.

XX Lowery DE, Geary TG, Kubiak TM, Larsen MJ;

XX WPI; 2001-343952/36.

XX P-PSDB; AAU03852.

PT Using G-protein-coupled receptor (GPCR)-like receptors to identify  
PT candidate compounds for the treatment and prevention of invertebrate  
PT parasites, especially helminths and insects.

XX Claim 1; Page 177-178; 219pp; English.

XX The sequence represents a DNA encoding a G protein-coupled receptor-like  
CC (GPCR-like) receptor protein. GPCR-like receptors and their associated  
CC nucleic acids may be used to identify candidate compounds for their  
CC ability to modulate the activity of GPCRs. The sequences therefore are  
CC useful for treating and preventing infection by endoparasitic and  
CC ectoparasitic invertebrate parasites, especially helminths and insects,  
CC and particularly ailments related to aberrant neurological and  
CC neuromuscular function

XX Sequence 1301 BP; 353 A; 304 C; 286 G; 358 T; 0 U; 0 Other;

Query Match 93.0%; Score 1109; DB 4; Length 1301;  
Best Local Similarity 94.2%; Pred. No. 0;  
Matches 1193; Conservative 0; Mismatches 0; Indels 74; Gaps 1;

QY 1 ATGGTTAGTTTCGGCGCCACCATTTTCGACCATTTTCAACACACAGCTCCCTCCACCATC 60  
DB |||||  
QY 1 ATGGTTAGTTTCGGCGCCACCATTTTCGACCATTTTCAACACACAGCTCCCTCCACCATC 60  
DB |||||  
QY 61 AGCAACGTTATCACAAGTCATTTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120  
DB |||||  
QY 61 AGCAACGTTATCACAAGTCATTTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120  
DB |||||  
QY 121 GCGGCACAAGGCATCGATGATATTTACTGTAGACTTTTATCATCCGATCAATCTTTCATTC 180  
DB |||||  
QY 121 GCGGCACAAGGCATCGATGATATTTACTGTAGACTTTTATCATCCGATCAATCTTTCATTC 180  
DB |||||  
QY 181 CTCTACGGGTTCTGTTTGTATTTAGGCAATTTTGGAAACGGCGGCTACTATGGGCGGTG 240  
DB |||||  
QY 181 CTCTACGGGTTCTGTTTGTATTTAGGCAATTTTGGAAACGGCGGCTACTATGGGCGGTG 240  
DB |||||

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QY 241 GCGAGAAACAGCGCTCCAACTCGCTCGCAACGATATTTCTGCTCAACTTGATCTTCACC 300
Db 241 GCGAGAAACAGCGCTCCAACTCGCTCGCAACGATATTTCTGCTCAACTTGATCTTCACC 300
QY 301 GATTGTGATATTTGGTGTTCACAGCGATTCAGTCAACCATGTTACGGGATGACCAAGAC 360
Db 301 GATTGTGATATTTGGTGTTCACAGCGATTCAGTCAACCATGTTACGGGATGACCAAGAC 360
QY 361 TGGGATTCGGGTGATGATGCAATTTAGTTCCTTGTGCAATTCGTTCGGTGTTC 420
Db 361 TGGGATTCGGGTGATGATGCAATTTAGTTCCTTGTGCAATTCGTTCGGTGTTC 420
QY 421 GTGACGAGTTCGAGCCTCACTGCAATCTCTTGTGATAAATTTCTGCAATCAACGATCCC 480
Db 421 GTGACGAGTTCGAGCCTCACTGCAATCTCTTGTGATAAATTTCTGCAATCAACGATCCC 480
QY 481 ACCAAACACAGATTTCTTATTCGTCAAGCGTTGGCAATTAACATTTCTTATCTGGATGTC 540
Db 481 ACCAAACACAGATTTCTTATTCGTCAAGCGTTGGCAATTAACATTTCTTATCTGGATGTC 540
QY 541 TCAACATGATATAATCTACCGTATCTTATGCTTTTCGAGCAGCTCGATGGAAGCTTTTAC 600
Db 541 TCAACATGATATAATCTACCGTATCTTATGCTTTTCGAGCAGCTCGATGGAAGCTTTTAC 600
QY 601 GTTCAGCCCGAGAACTCCATCTGCGGCACTTTTCGACGAGCGGCAATTTGGCAGAGC 660
Db 601 GTTCAGCCCGAGAACTCCATCTGCGGCACTTTTCGACGAGCGGCAATTTGGCAGAGC 660
QY 661 GAAATAGTCGAAAGATTTACGGAACTACGGTATATGTTTACAGTTCGTGTCGGATG 720
Db 661 GAAATAGTCGAAAGATTTACGGAACTACGGTATATGTTTACAGTTCGTGTCGGATG 720
QY 721 GAGTGATCAGTATGCTATCTTCAAAATCTTGCAAAAGTGTCAAAAGACATGATCATC 780
Db 721 GAGTGATCAGTATGCTATCTTCAAAATCTTGCAAAAGTGTCAAAAGACATGATCATC 780
QY 781 CAAATGCTCAATCTGTCATCTGACACAAAGAGAGAGAGTGTGCGACGTCACGA 840
Db 781 CAAATGCTCAATCTGTCATCTGACACAAAGAGAGAGAGTGTGCGACGTCACGA 840
QY 841 AAGAGAAAGTGAATATATTTCTAATGCAATGTTGTGACATTTATCGGGTGTGGTGG 900
Db 841 AAGAGAAAGTGAATATATTTCTAATGCAATGTTGTGACATTTATCGGGTGTGGTGG 900
QY 901 CTTTAACTACTACTCAATTTGGTCAAGATTTTAAAGAGCCCGAATGGCTAAACGT 960
Db 901 CTTTAACTACTACTCAATTTGGTCAAGATTTTAAAGAGCCCGAATGGCTAAACGT 960
QY 961 CAGCGGTTCTTCTGGGCAATAAATGCTCAGCTCATAGCCATGCTTGTAGTCTGTGGAAC 1020
Db 961 CAGCGGTTCTTCTGGGCAATAAATGCTCAGCTCATAGCCATGCTTGTAGTCTGTGGAAC 1020
QY 1021 CTTCTGCTATTTCTTTTGGCTGACAGAAACAAACGTTCCGGACTGTCAAAAATATCTC 1080
Db 1021 CTTCTGCTATTTCTTTTGGCTGACAGAAACAAACGTTCCGGACTGTCAAAAATATCTC 1080
QY 1081 AACTCAACAG----- 1090
Db 1081 AACTCAACAGAGATTTGTCTCGTTTGGCCAGTAGAGTGAATCTCGATTCGGCGGTCA 1140
QY 1091 -----AGGTTCCAAAAGACAGTGGTCTGATTTGGAG 1126
Db 1091 -----AGGTTCCAAAAGACAGTGGTCTGATTTGGAG 1126
QY 1141 AGTTTCGAGAGAAACAATATGACAGGGTTCAAAAAGACAGTGGTCTGATTTGGAG 1200
Db 1141 AGTTTCGAGAGAAACAATATGACAGGGTTCAAAAAGACAGTGGTCTGATTTGGAG 1200
QY 1127 GGATCCAGCTACAGACCTCTCCGACCTCTACTCATTTCCGACAGATGTGCGAGCAACT 1186
Db 1127 GGATCCAGCTACAGACCTCTCCGACCTCTACTCATTTCCGACAGATGTGCGAGCAACT 1186
QY 1187 CTTTCTA 1193
Db 1187 CTTTCTA 1267
```

## RESULT 4

AAS07210  
ID AAS07210 standard; DNA; 1130 BP.

XX AAS07210;

XX AC

XX AC

DT 12-SEP-2001 (first entry)

XX G protein-coupled receptor-like (GPCR-like) receptor DNA #10.

XX G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;

XX endoparasite; ectoparasite; invertebrate; insect; neurological disorder;

XX neuromuscular disorder; human; nematode; ds.

XX Homo sapiens.

XX WO200138533-A2.

XX 31-MAY-2001.

XX 24-NOV-2000; 2000WO-US032225.

XX 24-NOV-1999; 99US-0167523P.

XX (PHAA ) PHARMACIA & UPJOHN.

XX Lowery DE, Geary TG, Kubiak TM, Larsen MJ;

XX WPI; 2001-343952/36.

XX P-PSDB; AAU03811.

XX Using G-protein-coupled receptor (GPCR)-like receptors to identify

XX candidate compounds for the treatment and prevention of invertebrate

XX parasites, especially helminths and insects.

XX Claim 1; Page 116-118; 219pp; English.

XX The sequence represents a DNA encoding a G protein-coupled receptor-like

XX (GPCR-like) receptor protein. GPCR-like receptors and their associated

XX nucleic acids may be used to identify candidate compounds for their

XX ability to modulate the activity of GPCRs. The sequences therefore are

XX useful for treating and preventing infection by endoparasitic and

XX ectoparasitic invertebrate parasites, especially helminths and insects,

XX and particularly ailments related to aberrant neurological and

XX neuromuscular function

XX SQ Sequence 1130 BP; 340 A; 241 C; 225 G; 324 T; 0 U; 0 Other;

Query Match 8.1%; Score 96.6; DB 4; Length 1130;

Best Local Similarity 47.0%; Pred. No. 1.1e-18;

Matches 438; Conservative 0; Mismatches 454; Indels 39; Gaps 3;

QY 136 GATGATATTAATCTAGTACTTTTACATCCGATCAATTTTCAATCTCTACGGGTTCCCTG 195

Db 52 GAAGATTGTTCATCAAGGTGGTACATAATGTTAGTGTTCATTTCTCTACCTGATAATC 111

QY 196 TTTGTATTTAGGATTTTGGAAACGGCGGCTACTATCGGCGGTGGCGAACAACGCGG 255

Db 112 ATTCGCGCGGAATAATTTGGAACCTCATGTGTGATTTTGGCAATCACAAGGAACAATCA 171

QY 256 CTCCAATCGGCTCGCAACGATTTTCTGCTCAACTTGAATTTTCCCGATTTTGATTTGGTG 315

Db 172 CTTCAACTGTTCCGAACTGTTTATTTCTTTTATCATGTTCTGATATTTGTTGATGC 231

QY 316 TTCAAGCGATTTCCAGTCAACCAATGTTACCGGATGACCAAGACTGGGCTATCCGGTCA 375

Db 232 TGACATCTGCAACAATCACTCGATTTACTGCAATTTCAAGAAAGATGATCTTTGGAGAG 291

QY 376 GTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTTGGTGTGACGAGTTGGAGC 435

Db 292 GCTTTATGCGGAATTTGCACCAATTCATGCTGGTATCAGCCTTTGTTCTCAACTTTCACA 351

QY 436 CTCCTGCAATCTCCTTAGATAAAATTTCTGCATATATCAACGATCCCAACCAACACAGTT 495

352 TTGACTGCAATCTCCATCGACGATACATCTGATTCGATTTCCGATGAGGAACCTATT 411  
496 TCTATTCTGCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTCTCAACACTGATAAAT 555  
412 ACGCAATTATCAAGCGTTGGAGTGATTCGATTAATTTTGGCTTTGCTGCAACCACTCA-- 469  
556 CTACCGTATCTTATGCTTTTCGAGCAGCGTGATGGAAGCTTTTACGTTTCAGCCCGGAGAA 615  
470 ----CATCCCAATAATGTTCAAGCAAAAGCTGGAGAGTTTGAGAAAT----- 513  
616 ACTCCATATCTGGCGGCACTTTTCGAGCAGGCGGAATTTGCAGAGCGAAATAGTCGAAG 675  
514 -----TTTGTGGGCGAGTACTCGAGGAAACTGGGGAGCCAAATGAAGCCGAGAGAAA 567  
676 ATTTACGGAACACTACGGTTATGTTTACAGTTTCGTCGTCGATGGCAGTGATCAGGTAT 735  
568 ATTATGTTGTCAGCTCTGATGTTTCTTACGTCGTCATTCGCGCTTACCATCATCATATA 627  
736 TGTCTACTTCAAAATCTTGCAAAAGTGTCAAAAGCATGATCATCAAAATGCTCAATTC 795  
628 TCTACACTGCGGATTTCTTTGAAGATCGGACAAAGCATGATTTCTCAAGGGGCGGAAAAAG 687  
796 TGTCAATCACTGA-----CACAAAAGCAGAGAGTGTGCGACGTCAACA 840  
688 CAAAAGCAGACAAATTTGGGAATGGAATTAAGTGATCAACAAGAAATCGCTGTGAAGAGA 747  
841 AAGAAGAAAGTGAATPATATTTCTTAATGCAATGTTGTGCACATTTATTCGGGTGTTGGTTG 900  
748 AGACAAAGAACTAATAGATGCTTATTTGGTATGTTAGTCGCAATTCGCTTGGCAGCTGGATT 807  
901 CTTTAACTATTAATCAATTTGTTGCAAGATTTTAAAGAGAGCCGGAATGGCTTAAACGT 960  
808 TGGTCAGTGCAGTTCAACATTTCTGAGGAGCTATGAATATTTGCCAGAGCTCATCAAACT 867  
961 CAGCGGTTCTTCTGGGCAATAAATGCTCAGTCATAGCCATGCTCTTACTGCTCTGGAC 1020  
868 CAAGATATATCTTTGGAAATGCTACACATTCGATTTGCAATGACCTCAACGGTATGGAAC 927  
1021 CCTCTGCTATTTCTTTGGCTGACGAGAAAC 1051  
928 CCGTTACTCTACGAGTGTCAACCTCCAAC 958

## RESULT 5

AAS07217  
ID AAS07217 standard; DNA; 1098 BP.

AC AAS07217;

XX 12-SEP-2001 (first entry)

DE G protein-coupled receptor-like (GPCR-like) receptor DNA #17.

XX G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;  
KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;  
KW neuromuscular disorder; human; nematode; ds.

OS Homo sapiens.

XX WO200138533-A2.

XX 31-MAY-2001.

XX 24-NOV-2000; 2000WO-US032225.

XX 24-NOV-1999; 99US-0167523P.

XX (PHAA ) PHARMACIA & UPJOHN.

XX Lowery DE, Geary TG, Kubiak TM, Larsen MJ;

XX WPI; 2001-343952/36.

DR P-PSDB; AAU03818.

XX Using G-protein-coupled receptor (GPCR)-like receptors to identify  
PT candidate compounds for the treatment and prevention of invertebrate  
PT parasites, especially helminths and insects.

XX Claim 1; Page 139-141; 219pp; English.

XX The sequence represents a DNA encoding a G protein-coupled receptor-like  
CC (GPCR-like) receptor protein. GPCR-like receptors and their associated  
CC nucleic acids may be used to identify candidate compounds for their  
CC ability to modulate the activity of GPCR. The sequences therefore are  
CC useful for treating and preventing infection by endoparasitic and  
CC ectoparasitic invertebrate parasites, especially helminths and insects,  
CC and particularly ailments related to aberrant neurological and  
CC neuromuscular function

XX Sequence 1098 BP; 280 A; 250 C; 230 G; 338 T; 0 U; 0 Other;

XX Query Match 7.0%; Score 84; DB 4; Length 1098;

XX Best Local Similarity 50.5%; Pred. No. 8.7e-15;

XX Matches 204; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

QY 167 CAATCTTCACTTCTCTACGGTTCCTGTTGTTATAGGCATTTTGGAAAGCGCGG 226

DB 86 CGATTCTTGGCAACCATCTACACTATAATTTGTCGTAGTTGGCGTAACCGCAATTTGTTAG 145

QY 227 TACTATGGCGGTGGCGAGAAACAAAGCGGCTCCAATCGGCTCGCAACGTTATTTCTGCTCA 286

DB 146 TAGTGATGTGGGTGATGAGGTTCAAGTCTTCAATCATGTCAGGAACATGTTTCATCGTAT 205

QY 287 ACTTGATCTTCAACGATTTGATTAATTTGTTTTCACAGCGATTCCAGTCACACCATGGTAGC 346

DB 206 CTTTGTGAGTTTCTGACATTTTGTGGCGATTTGTTAGTGGTTTCAGTAACCGCGATAACCG 265

QY 347 CGATGACCAAGACTGGGCATTTGGGTGAGTGATGTCATTTAGTCTTCTTGTCAAAT 406

DB 266 CATTCTCTAAGTTTGGTTATTTGGTGACCAATTTGTGTCTTACTACTCTTTGTTACAGG 325

QY 407 CGTGTTCGTGTTTGTGACGAGTTTGGAGCCTCAGTCGCAATCTCTTAGATAAATTTCTGCG 466

DB 326 GTACCGCGTTGAGTTTTCACGTTAACGCTCACCGCAATTGCAATTTGACAGATATATTC 385

QY 467 ATATCAACGATCCCAACCAACACAGTTTCTTATTCGTCAAGCGTTGGCAATTAACATTTTC 526

DB 386 TCATCTGTCTCGAGCAAGAACCGATACGCAAAAGATCAAGCATTGAAAATGATAAGTT 445

QY 527 TTATCTGATAGTCTCAACACTGATAAATCTACCGTATCTTATG 570

DB 446 TCAACAGCGCCATCTCAGTTGGGCTTTCGGTACCAATTTATTCATG 489

## RESULT 6

AAS07208

ID AAS07208 standard; DNA; 1352 BP.

XX AAS07208;

XX 12-SEP-2001 (first entry)

DE G protein-coupled receptor-like (GPCR-like) receptor DNA #8.

XX G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;  
KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;  
KW neuromuscular disorder; human; nematode; ds.

OS Homo sapiens.

XX WO200138533-A2.

XX 31-MAY-2001.

XX 24-NOV-2000; 2000WO-US032225.

```
XX 24-NOV-1999; 99US-0167523P.
PR (PHAA ) PHARMACIA & UPJOHN.
PA Lowery DE, Geary TG, Kubiak TM, Larsen MJ;
XX WPI; 2001-343952/36.
XX P-PSDB; AAU03809.
XX Using G-protein-coupled receptor (GPCR)-like receptors to identify
XX candidate compounds for the treatment and prevention of invertebrate
XX parasites, especially helminths and insects.
XX Claim 1; Page 108-110; 219pp; English.
XX The sequence represents a DNA encoding a G protein-coupled receptor-like
XX (GPCR-like) receptor protein. GPCR-like receptors and their associated
XX nucleic acids may be used to identify candidate compounds for their
XX ability to modulate the activity of GPCRs. The sequences therefore are
XX useful for treating and preventing infection by endoparasitic and
XX ectoparasitic invertebrate parasites, especially helminths and insects,
XX and particularly ailments related to aberrant neurological and
XX neuromuscular function
XX Sequence 1352 BP; 337 A; 284 C; 307 G; 424 T; 0 U; 0 Other;
XX Query Match 6.6%; Score 78.8; DB 4; Length 1352;
XX Best Local Similarity 47.4%; Pred. NO. 3.9e-13;
XX Matches 381; Conservative 0; Mismatches 402; Indels 21; Gaps 4;
QY 134 TCGATGATATTACTGTAGACATTTTACATCCGATCATCTTCACATTCCTCTACGGGTCC 193
DB 56 TCAATGATTGGACAGTCTCTTTGAAGTTCGGCTTGGATATTCAGTACTATCTTCTCA 115
QY 194 TGTGTGTTATTAGGCATTTTGGAAACGGCGGTACTATGGCGGTGGCGAGAAACAAGC 253
DB 116 TATTAAATATCGGATTGGTGGAAATGGCTATTGATCACTTCATTTTAAATCGAAGA 175
QY 254 GGCTCAATCGGCTCGCAAGTATTTCTGCTCAACTTGATCTTCAACGATTTGATTTGG 313
DB 176 AACTTTCGGTGGC---AAACATATTCTTGATAAACCTGGCAGTTTCTGATTTGCTTCTT 232
QY 314 TGTTCACAGCGATTCACATCCACCATGGTAGCGATGACCAAGACCTGGGATTCGGGT 373
DB 233 GCATCAGCGCGGTGCGGATCACTCCAGTATGGCGTTTATGAAGCGATGGATATTTGGA 292
QY 374 CAGTCATGTGCCATTTAGTTCCTTTGTCAAATTCGTTCGGTGTTCGTGACGAGTTGGA 433
DB 293 TAAATATGTGTAATTTGTTCCAACTTGTCCAGGCGTTTTCGGTCTCATTTCTTCATGT 352
QY 434 GCCTCACTGCAATCTCTTAGATAAATTTTCGATATCAACGATCCACCAACAACACGAG 493
DB 353 CTTTGTGTATCATCGCAATTTGATAGATATCGAAGTATTTGACGCGCACTCCGGGAACCAT 412
QY 494 TTTCTATTTCGTCAGCGTTGGCAATACTTTCTTCGATCTCTGATCTTCAACACTGATA 553
DB 413 GGTCTGATAGGATGCAAGGTGGCTTCTGATGTTCAATGGGTGGTGGCTTCTTCTGCTA 472
QY 554 ATCTACCGTATCTTATGTCCTTCGAGCACGTCGATGGAAGCTTTTACGTTTCAGCCGGAG 613
DB 473 GT-----TATCTCTATATTAATCAAGAACTTTGAACAAATGTTATTGA-----AA 520
QY 614 AAATCCCATATCGCGGCACTTTTCGACGAGCGGAAATTTGGCAGAGCGAAATATGTCGAA 673
DB 521 ATGTGACATTAATGTGAGATTTTTCGGCGAGTTCAATTTGGCAGTCGGATGAATATCCA 580
QY 674 AGATTTACGGAACACTAGGTATTTGTTTACAGTTTCGTCTGCGGATGGCAGTATCACT 733
DB 581 AGTTGACATATACAGAGTTTATTGAATATTCAGCTGATTAATTCAGCAATATATCATGT 640
QY 734 ATTGCTACTTCAAAATCTTGCAGAAAGTGTCAAAGACATGATCATCAAAATGCTCAAT 793
641 CTTTGTGTTATTTAATGATTTCTACAAAGGTACAAACCGACTGGCTTGTGACGAGGAT 700
QY 794 TCTGTCAATCACTGACACAAAAGCAGAGAAGTATGCGAGTCAAGAAAGAAAGTGA 853
DB 701 CCATGTTGACTGCGCGCAACAGGCTCAACAGCAG-----TTCGAAGCGCAGAGTGA 754
QY 854 ATTATATTCTAAATTCGAATGTTGTTCACATTTATTCGGGTGTTGGTTGCTTTAAACATTAC 913
DB 755 TGTACGTTGTTGATTTCTAATGTTATGTTTATGCTTGTGCTTCCGTTGTCGCGCG 814
QY 914 TCAATTTGGTCAAGAGATTTTAAAA 937
DB 815 TGAATTTGTTCAAGAGATCTCGAA 838
RESULT 7
AAS07212
ID AAS07212 standard; DNA; 1374 BP.
XX AC AAS07212;
XX AC AAS07212;
XX DT 12-SEP-2001 (first entry)
XX DE G protein-coupled receptor-like (GPCR-like) receptor DNA #12.
XX DE G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
XX KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
XX KW neuromuscular disorder; human; nematode; db.
XX OS Homo sapiens.
XX PN WO200138533-A2.
XX PD 31-MAY-2001.
XX PF 24-NOV-2000; 2000WO-US032225.
XX PR 24-NOV-1999; 99US-0167523P.
XX PA (PHAA ) PHARMACIA & UPJOHN.
XX PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;
XX WPI; 2001-343952/36.
XX P-PSDB; AAU03813.
XX Using G-protein-coupled receptor (GPCR)-like receptors to identify
XX candidate compounds for the treatment and prevention of invertebrate
XX parasites, especially helminths and insects.
XX Claim 1; Page 122-124; 219pp; English.
XX The sequence represents a DNA encoding a G protein-coupled receptor-like
XX (GPCR-like) receptor protein. GPCR-like receptors and their associated
XX nucleic acids may be used to identify candidate compounds for their
XX ability to modulate the activity of GPCRs. The sequences therefore are
XX useful for treating and preventing infection by endoparasitic and
XX ectoparasitic invertebrate parasites, especially helminths and insects,
XX and particularly ailments related to aberrant neurological and
XX neuromuscular function
XX Sequence 1374 BP; 402 A; 280 C; 296 G; 396 T; 0 U; 0 Other;
XX Query Match 5.6%; Score 66.6; DB 4; Length 1374;
XX Best Local Similarity 48.3%; Pred. NO. 2.3e-09;
XX Matches 186; Conservative 0; Mismatches 199; Indels 0; Gaps 0;
QY 180 CCTCTACGGTTCCTGTTGTTGTTATAGGCAATTTTGGAAACGGCGGCTACTATGGCGGT 239
DB 93 CGTGACCTTTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 152
QY 240 GCGCGAGAAACAAGCGCGCTCCAAATCGGCTCGCAACGATTTTCTGCTCAACTGATCTTCA 299
```









PT CDS 31..1293  
 FT /\*tag= a  
 FT /product= "Human neuropeptide FF2 (NPFF2) receptor  
 FT protein"  
 XX US6849727-B1.  
 XX 01-FEB-2005.  
 XX 29-MAR-2000; 2000US-00538036.  
 XX 25-SEP-1998; 98US-00161113.  
 XX 22-FEB-1999; 99US-00255368.  
 XX 24-SEP-1999; 99US-00405558.  
 XX (LUND ) LUNDBECK AS H.  
 XX Gerald CPG, Jones KA, Bonini JA, Borowsky BE, Craig DA;  
 XX WPI, 2005-129971/14.  
 XX P-PSDB; ADM80002.  
 XX New nucleic acid encoding a human or rat neuropeptide FF2 receptor,  
 XX useful for diagnosing or treating a disorder, e.g. cardiovascular,  
 XX affective, reproductive, gastrointestinal, or lower urinary tract  
 XX disorders.  
 XX Disclosure; SEQ ID NO 5; 95pp; English.  
 XX PS  
 XX The present invention relates to a neuropeptide FF (NPFF) receptor  
 XX proteins and their DNA. The invention is useful for diagnosing or  
 XX treating a disorder, e.g. diuresis, cardiovascular conditions such as  
 XX hypertension, hypotension and congestive heart failure, memory loss,  
 XX affective disorders, schizophrenia, pain, locomotor problems, circadian  
 XX rhythm disorders, eating/body weight disorders, sexual/reproductive  
 XX disorders, nasal congestion, diarrhea, gastrointestinal disorders, or  
 XX disorders of the lower urinary tract. The invention is also useful in  
 XX gene therapy. The present sequence is the human neuropeptide FF2 (NPFF2)  
 XX receptor protein encoding DNA.  
 XX SQ Sequence 1302 BP; 381 A; 303 C; 263 G; 355 T; 0 U; 0 Other;  
 Query Match 5.2%; Score 61.6; DB 14; Length 1302;  
 Best Local Similarity 46.3%; Pred. No. 8e-08; Mismatches 234; Indels 0; Gaps 0;  
 Matches 202; Conservative 0;  
 QY 165 ATCAATCTTCACATTCCTCTACGGTTCCTGTTGTTGTTAGGCAATTTTGGAAACGGCGG 224  
 DB |||||  
 QY 165 AGCAATCTTCATTAATTCCTACTCTTCTGATCTCTTTTGTGATGATGGGAATACTGT 224  
 DB |||||  
 QY 225 CGTACTATGGCGGTGGCGAGAAACAGCGGCTCCAAATCGGTCGGAACGTAATTTCTGCT 284  
 DB |||||  
 QY 225 GGTTCGCTTAATGTAATGAGGAACAAACATATGCACAGTCACTAATCTCTTCATCTT 284  
 DB |||||  
 QY 285 CAATCTGATCTTCACGATTCGATTTGTTGTTGTTCCAGGATTCAGTCACACCATGGTA 344  
 DB |||||  
 QY 285 AAACCTGGCCATAAGTATTTACTAGTTGGCAATTTCTGCATGCCCTAATACACTGCTGA 344  
 DB |||||  
 QY 345 CGCGATGACAAAGACTGGGCAATTCGGGTCACTGATGTGCCAATTTAGTTCTTTGTCAA 404  
 DB |||||  
 QY 345 CAATATTAGCAGGATGCCAATTTGGAACAGATGTGCAAGATCAGTGGATTTGTCCA 404  
 DB |||||  
 QY 405 TTCGTGTTGGTGTGTCAGAGTTGGAGCCTCACTGCATCTCTCTAGATAAATTTCT 464  
 DB |||||  
 QY 405 GGGAAATATCTGTCGAGCTTCAGTCTTTACGTTAGTTGCAATTTGCTGTAGATAGGTTCA 464  
 DB |||||  
 QY 465 GCATATCAAGATCCACCAACACACAGTTTCTATTCGTCAGCGTTCGCAATACAT 524  
 DB |||||  
 QY 465 GTGTGTGCTTACCTTTTAAACCAAGCTCACTATCAAGACAGCGTTTGTCAATTAAT 524  
 DB |||||  
 QY 525 TCTTATCTGGATGCTCAACACTGTATAATCTACCGTATCTTATGTTCTTTCGACACGT 584  
 DB |||||  
 QY 525 GATCATCTGGTCTTAGCCATCACCATTAATGTTCCATCTGCAGTAATGTTACATGTGCA 584  
 DB |||||

QY 585 CGATGAAGCTTTTAC 600  
 DB |||||  
 DB 585 AGAAGAAAATATTAC 600  
 RESULT 13  
 ADZ76145  
 ID ADZ76145 standard; DNA; 1302 BP.  
 XX AC ADZ76145;  
 XX 14-JUL-2005 (first entry)  
 XX Human neuropeptide FF receptor (NPFF2b) DNA, SEQ ID NO: 5.  
 XX Neuropeptide FF receptor; urinary tract disease; uropathic;  
 XX antiinflammatory; genitourinary disease; gastrointestinal disease;  
 XX gastrointestinal-gen.; cardiovascular disease; cardiovascular-gen.;  
 XX hypotensive; hypertensive; antidiabetic; metabolic disorder;  
 XX respiratory disease; respiratory-gen.; antiasthmatic; inflammation;  
 XX genitourinary disease; immune disorder; immunomodulator;  
 XX endocrine disease; endocrine-gen.; musculoskeletal disease;  
 XX muscular-gen.; osteopathic; cognitive disorder; nootropic;  
 XX neurological disease; memory disorder; anorectic; nutritional disorder;  
 XX analgesic; antismoking; psychiatric disorder; toxicity and intoxication;  
 XX antiaddictive; antimigraine; gene; ds.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT CDS 31..1293  
 FT /\*tag= a  
 FT /product= "Human NPFF receptor (NPFF2b) protein"  
 XX US2005089937-A1.  
 XX 28-APR-2005.  
 XX 18-NOV-2004; 2004US-00992407.  
 XX 25-SEP-1998; 98US-00161113.  
 XX 22-FEB-1999; 99US-00255368.  
 XX 24-SEP-1999; 99US-00405558.  
 XX 29-MAR-2000; 2000US-00538036.  
 XX (GERA/) GERALD C P G.  
 XX (JONE/) JONES K A.  
 XX (BONI/) BONINI J A.  
 XX (BORO/) BOROWSKY B E.  
 XX (CRAI/) CRAIG D A.  
 XX Gerald CPG, Jones KA, Bonini JA, Borowsky BE, Craig DA;  
 XX WPI; 2005-344283/35.  
 XX P-PSDB; ADZ76146.  
 XX Preparing a composition that specifically binds to mammalian neuropeptide  
 XX FF (NPFF) receptor, comprises determining if the compound is a mammalian  
 XX NPFF receptor agonist, recovering the compound and admixing a carrier.  
 XX Disclosure; SEQ ID NO 5; 103pp; English.  
 XX The invention relates to a method for preparing a composition that  
 XX specifically binds to mammalian neuropeptide FF (NPFF) receptor. The  
 XX method involves determining whether the compound is a mammalian NPFF  
 XX receptor agonist, recovering the compound and admixing a carrier. The  
 XX method is useful for preparing a composition which specifically binds to  
 XX mammalian NPFF receptor. The composition is used to treat e.g. a lower  
 XX urinary tract disorder such as interstitial cystitis or urinary  
 XX incontinence, a gastrointestinal disorder, irritable bowel syndrome, a  
 XX cardiovascular disorder, hypertension, hypotension, diabetes,  
 XX hypoglycemia, a respiratory disorder, asthma, a reproductive function

CC disorder, an immune disorder, an endocrine disorder, a musculoskeletal  
CC disorder, a cognitive disorder, a memory disorder, obesity, pain,  
CC nicotine addiction, opiate addiction or migraine. The present sequence is  
CC the human NPPF receptor (NPPF2b; NPPF2) DNA.

XX SQ Sequence 1302 BP; 381 A; 303 C; 263 G; 355 T; 0 U; 0 Other;

Query Match 5.2%; Score 61.6; DB 14; Length 1302;

Best Local Similarity 46.3%; Pred. No. 8e-08;

Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

QY 165 ATCAATCTTCAATCTCTACGGTTCCTGTTTGTATAGGCAATTTTGGAAACGGCGG 224

DB 165 AGCAATCTTCAATCTCTACGGTTCCTGTTTGTATAGGCAATTTTGGAAACGGCGG 224

QY 225 CGTACTATGGCGGTGGGAGAAACAGCGGCTCCAAATCGGCTCGCAAGTATTTCTGCT 284

DB 225 GGTTCGCTTATTTGTAATGAGGAACAAACATATGCAACAGTCACTAAATCTCTTCATCT 284

QY 285 CCACTTGTATCTTCAACGATTTGATATTTGGTGTTCACAGGATTCAGTCACACATGTA 344

DB 285 AAACCTGGCCATTAAGTATTTAGTGGCATATTTCTGCATGCCCTATAACACTGCTGA 344

QY 345 CGCGATGACCAAGACTGGGCAATTCGGGTCAAGTGTGCAATTTAGTTCCTTTGTCAAA 404

DB 345 CAATATTAAGCAGGATGCCATTTGGAAACAGATGTGCAAGATCAGTGGATGTGCTCA 404

QY 405 TTGCTGTTGGTGTGAGCGAGTTGGAGCCCTCACTGCAATCTCCTTAGATAAAATTTCT 464

DB 405 GGGAAATATCTGTGCGAGCTTCACTCTTTAGCTTGTGCAATTTGCTGTAGATAGTTC 464

QY 465 GCATATCAACGATCCCAACCAACAGCTTCTATTCGTCAGCGTTGGCAATACATTT 524

DB 465 GTGTGTGGTCTACCTTTTAAACCAAGCTCACTATCAAGACAGCGTTTGTCAATTTAT 524

QY 525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGCTCTTTTCAGCAC 584

DB 525 GATCATCTGGTCCCTAGCCATCACCATTATGCTCCATCTGCAGTATGTTACATGTGCA 584

QY 585 CGATGGAAGCTTTTAC 600

DB 585 AGAAGAAAAATATTAC 600

RESULT 14

AAA57839  
ID AAA57839 standard; DNA; 1440 BP.

XX AC

XX AAA57839;

XX DT 20-OCT-2000 (first entry)

XX DE DNA encoding a human A4 receptor polypeptide.

XX KW Human; G protein coupled receptor; A4 receptor; cell line; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT 121..1383

XX FT /\*tag= a

XX FT /product= "A4 receptor"

XX CA2284857-A1.

XX PD 16-APR-2000.

XX PF 15-OCT-1999; 99CA-02284857.

XX PR 16-OCT-1998; 98US-00104514.

XX PR 16-OCT-1998; 98US-00173565.

XX PA (ALIX ) ALLELIX BIOPHARMACEUTICALS INC.

XX

XX Zastawny RL;

XX PI

XX DR

XX WPI; 2000-491457/44.

XX P-PSDB; AAB07426.

XX PT

XX Novel polynucleotide encoding G protein coupled receptor A4, useful for

XX producing recombinant cell lines for discovering therapeutic agents that

XX modulate the receptor activity.

XX PS

XX Claim 2; Fig 1; 59pp; English.

XX CC

XX The present sequence encodes a human G protein coupled receptor A4. The

XX A4 polynucleotide is found in adult human kidney, liver, lung, and

XX placenta. The receptor shows homology to the orexin receptor family. The

XX A4 polynucleotide sequence is useful for producing recombinant cell lines

XX that have commercial significance in discovering therapeutic compounds

XX that modulate the receptor activity

XX SQ

Sequence 1440 BP; 415 A; 334 C; 300 G; 391 T; 0 U; 0 Other;

Query Match

Best Local Similarity

Matches 202; Conservative

0; Mismatches 234; Indels

0; Gaps

0;

QY

165 ATCAATCTTCAATCTCTACGGTTCCTGTTTGTATAGGCAATTTTGGAAACGGCGG 224

DB

255 AGCAATCTTCAATCTCTACGGTTCCTGTTTGTATAGGCAATTTTGGAAACGGCGG 224

QY

225 CGTACTATGGCGGTGGGAGAAACAGCGGCTCCAAATCGGCTCGCAAGTATTTCTGCT 284

DB

315 GGTTCGCTTATTTGTAATGAGGAACAAACATATGCAACAGTCACTAAATCTCTTCATCT 374

QY

285 CCACTTGTATCTTCAACGATTTGATATTTGGTGTTCACAGCGATTCACAGTCAACATGTA 344

DB

375 AAACCTGGCCATTAAGTATTTAGTGGCATATTTCTGCATGCCCTATAACACTGCTGA 434

QY

345 CGCGATGACCAAGACTGGGCAATTCGGGTCAAGTGTGCAAGTGTGCAAGTGTGCAAG 404

DB

435 CAATATTAAGCAGGATGCCATTTGGAAACAGATGTGCAAGATCAGTGGATGTGCTCA 494

QY

405 TTGCTGTTGGTGTGAGCGAGTTGGAGCCCTCACTGCAATCTCCTTAGATAAAATTTCT 464

DB

495 GGGAAATATCTGTGCGAGCTTCACTCTTTAGCTTGTGCAATTTGCTGTAGATAGTTC 554

QY

465 GCATATCAACGATCCCAACCAACAGCTTTCATTCGTCAGCGTTGGCAATACATTTCT 524

DB

555 GTGTGTGGTCTACCTTTTAAACCAAGCTCACTATCAAGACAGCGTTTGTCTATTAT 614

QY

525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGCTCTTTTCAGCAC 584

DB

615 GATCATCTGGTCCCTAGCCATCACCATTATGCTCCATCTGCAGTAAATGTTACATGTGCA 674

QY

585 CGATGGAAGCTTTTAC 600

DB

675 AGAAGAAAAATATTAC 690

RESULT 15

ACH00816

ID ACH00816 standard; DNA; 1560 BP.

XX AC

XX ACH00816;

XX DT 12-FEB-2004 (first entry)

XX DE Human neuropeptide PF 2 coding sequence.

XX KW Energy homeostasis; mouse; metabolism; triglyceride; metabolic disease;

XX KW gene therapy; anorectic; immunomodulator; antidiabetic; hypotensive;

XX KW cardiant; osteopathic; antilipemic; gene; ds.

XX OS Homo sapiens.

XX WO2003075945-A2.  
XX 18-SEP-2003.  
XX 14-MAR-2003; 2003WO-EP002714.  
XX 14-MAR-2002; 2002EP-00005882.  
XX 15-MAR-2002; 2002EP-00006012.  
XX 20-MAR-2002; 2002EP-00006271.  
XX 25-MAR-2002; 2002EP-00006810.  
XX (DEVE-) DEVELOPEN ENTWICKLUNGSBIOLOGISCHE FORSCH.  
XX Eulenber K, Steuernagel A, Haeder T, Broenner G;  
XX MPI; 2003-748334/70.  
XX P-P8DB; ABG75056.  
XX New pharmaceutical composition comprising a nucleic acid molecule  
XX encoding proteins regulating the energy homeostasis and metabolism of  
XX triglycerides useful for detecting or preventing metabolic diseases, e.g.  
XX obesity.  
XX Claim 2; Fig 7B; 140pp; English.  
XX The present invention relates to pharmaceutical compositions comprising  
XX the coding sequences shown in ACH00815-ACH00827, or their encoded  
XX proteins (shown in ABG75054, ABG75056-ABG75067). These are proteins  
XX involved in the metabolism of triglycerides and in energy homeostasis,  
XX and their coding sequences. The composition is useful for the manufacture  
XX of an agent for detecting, verifying, treating, alleviating or preventing  
XX disorders, including metabolic diseases such as obesity and other body-  
XX weight regulation disorders as well as related disorders such as  
XX metabolic syndrome, eating disorder, cachexia, diabetes mellitus,  
XX hypertension, coronary heart disease, hypercholesterolaemia,  
XX dyslipidaemia, osteoarthritis or gallstones, in cells, cell masses,  
XX organs or subjects. The coding sequences can be used in the production of  
XX transgenic animals which under- or over-produce the gene of interest. The  
XX present sequence is a coding sequence of the invention  
XX  
XX Sequence 1560 BP; 476 A; 347 G; 287 G; 450 T; 0 U; 0 Other;  
Query Match 5.2%; Score 61.6; DB 10; Length 1560;  
Best Local Similarity 46.3%; Pred. No. 8.7e-08;  
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;  
QY 165 ATCAATCTTCACATTCCTCTACGGGTCTCTGTTGTTATTAGGCATTTTGGAAACGGCGG 224  
DB 182 AGCAATCTTCATATTTCCTACTCTTCTGATCTCTTTTGTGATGATGGGAATCTGT 241  
QY 225 CGTACTATGGCGGTGGGAGAAACAAGCGGTCCAAATCGGCTCGCAACGTATTTCTGCT 284  
DB 242 GGTTCGCTTTATTGTAATGAGGAACAACAATATGCACACAGTCACCTAATCTCTTCATCT 301  
QY 285 CAACCTTGATCTTCACCGATTGATATTTGTTGTTTCAGCGATTCAGTCACACCATGGTA 344  
DB 302 AAACCTGGCCATAAGTGAATTTACTAGTTGGCATATTTCTGCATGCCCTATAACACTGCTGGA 361  
QY 345 CGCGATGACCAAGACTGGGCATTCGGTCAGTGATGCCATTTAGTTCTTTTGCAAA 404  
DB 362 CAATATTTATGACGGATGCCATTTGGAAACAGATGTGCAAGATCAGTGGATTTGTCGA 421  
QY 405 TTCTGTTTCGGTGTGTTGTGACCGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAAATTTCT 464  
DB 422 GGGATATCTGTGCGAGCTTCAGTCTTTACGTTAGTTGCAATTTGCTGTAGTAGGTTCCA 481  
QY 465 GCATATCAACGATCCACCAACAACAGTTTCTATTCTCAAGCGTTGGCAATACATT 524  
DB 482 GTGTGTGGTCTACCCCTTTTAAACCAAGCTCACTCAAGACAGCGTTTGTCAATTATTAT 541  
QY 525 TCTTATCTCGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTTCGAGCAGCT 584

Db 542 GATCATCTGGGTCTCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCA 601  
Qy 585 CGATGGAAGCTTTTAC 600  
Db 602 AGAAGAAAAATATTAC 617  
Search completed: May 8, 2006, 14:50:30  
Job time : 815 secs



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Db 181 CTCTACGGGCTTCCTGTTGTTATTAGGCATTTTTTGGAAACGGCGGTACTATATGGCGGTG 240
Qy 241 GCGAGAAACAGCGGCTCAATCGGCTCGAACGTAATTTCTGCTCAACTGATCTTAC 300
Db 241 GCGAGAAACAGCGGCTCAATCGGCTCGAACGTAATTTCTGCTCAACTGATCTTAC 300
Qy 301 GATTTGATATTGGTGTTCACAGCGAATCCAGTCACACCATGTCAGCGATGACCAAGAC 360
Db 301 GATTTGATATTGGTGTTCACAGCGAATCCAGTCACACCATGTCAGCGATGACCAAGAC 360
Qy 361 TGGGCATTCGGGTCAAGTGTGCAATTTAGTTCCTTTTGTCAAAATCGTGTGGTGT 420
Db 361 TGGGCATTCGGGTCAAGTGTGCAATTTAGTTCCTTTTGTCAAAATCGTGTGGTGT 420
Qy 421 GTGACGAGTTGGAGCTCATCGCAATCTCTTAGATAAATTTCTGCATATCAACGATCCC 480
Db 421 GTGACGAGTTGGAGCTCATCGCAATCTCTTAGATAAATTTCTGCATATCAACGATCCC 480
Qy 481 ACCAAACACAGGTTTCTATTGTCAGCGGTTTGGCAATAACATTTCTTATCTGGATGTC 540
Db 481 ACCAAACACAGGTTTCTATTGTCAGCGGTTTGGCAATAACATTTCTTATCTGGATGTC 540
Qy 541 TCAACACTGATAAACTACCGTATCTTATGTCCTTTTCGAGCAGTCGATGGAAGCTTTTAC 600
Db 541 TCAACACTGATAAACTACCGTATCTTATGTCCTTTTCGAGCAGTCGATGGAAGCTTTTAC 600
Qy 601 GTTCAGCCGGAGAACTCCATACTGCGGGGCACTTTTGGAGCAGGCGAAATGGCAGAGC 660
Db 601 GTTCAGCCGGAGAACTCCATACTGCGGGGCACTTTTGGAGCAGGCGAAATGGCAGAGC 660
Qy 661 GAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTGTCGGATG 720
Db 661 GAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTGTCGGATG 720
Qy 721 GCAGTGATCAGCTATTTGCTACTTTCAAAATCTTGCAGGAGGTCGAAAGACATGATCATC 780
Db 721 GCAGTGATCAGCTATTTGCTACTTTCAAAATCTTGCAGGAGGTCGAAAGACATGATCATC 780
Qy 781 GAAATAGTCGAAATCTGTCATCTGACACAAAGCAGAGAGTGTGCGAGCTCAGCA 840
Db 781 GAAATAGTCGAAATCTGTCATCTGACACAAAGCAGAGAGTGTGCGAGCTCAGCA 840
Qy 841 AAGAAAGAGTGAATTTATTTCTAATGCAATGTTGTCACATTTATCGGTTGGTGTG 900
Db 841 AAGAAAGAGTGAATTTATTTCTAATGCAATGTTGTCACATTTATCGGTTGGTGTG 900
Qy 901 CCTTTAAACATTAATCTCAATTTGGTCAAGATTTTAAAAAGAGCCCGAATGGCTAAAAAGT 960
Db 901 CCTTTAAACATTAATCTCAATTTGGTCAAGATTTTAAAAAGAGCCCGAATGGCTAAAAAGT 960
Qy 961 CAGCGGTTCTTCTGGGCAATAAATGCTCAGGTCATAGCCATGCTCTTAGTCTGTGGAC 1020
Db 961 CAGCGGTTCTTCTGGGCAATAAATGCTCAGGTCATAGCCATGCTCTTAGTCTGTGGAC 1020
Qy 1021 CCTCTGCTATTCTTTTGGCTGACAGAAACAAAACGTTCCGGACTGTCAAAAATATCTC 1080
Db 1021 CCTCTGCTATTCTTTTGGCTGACAGAAACAAAACGTTCCGGACTGTCAAAAATATCTC 1080
Qy 1081 AACTCAACAGAGGGTTTCAAAAAGCAGGTGTTCTGGATTGCGAGGGATCCAGCTACAC 1140
Db 1081 AACTCAACAGAGGGTTTCAAAAAGCAGGTGTTCTGGATTGCGAGGGATCCAGCTACAC 1140
Qy 1141 GACCTCTCCGACCTCTACTCATTTCCGACAGATGTCAGGCACTCTTTCTA 1193
Db 1141 GACCTCTCCGACCTCTACTCATTTCCGACAGATGTCAGGCACTCTTTCTA 1193
```

## RESULT 2

US-10-650-467-39

; Sequence 39, Application US/10650467

; Publication NO. US20050176069A1

; GENERAL INFORMATION:

; APPLICANT: Lowery, David E.

```
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/10/650,467
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870
; PRIOR FILING DATE: CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 1500
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1497)
; FEATURE:
; OTHER INFORMATION: Clone identifier: CEGPCR19
US-10-650-467-39
```

Query Match 100.0%; Score 1193; DB 9; Length 1500;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 ATGTTAGTTCGGCGGCCACCAATTTGACGATTTCAACCAACGACTCCCTCCACCATC 60
Db 307 ATGTTAGTTCGGCGGCCACCAATTTGACGATTTCAACCAACGACTCCCTCCACCATC 366
Qy 61 AGCAACGTTATCACAAAGTCATTTCCGAAATGCTGTCATTCAGATCGCTGAGCGGAT 120
Db 367 AGCAACGTTATCACAAAGTCATTTCCGAAATGCTGTCATTCAGATCGCTGAGCGGAT 426
Qy 121 CGGCAACAGCATCGATGATATTAATCTGTAACATTTTACATCCGATCAATCTTCAATTC 180
Db 427 CGGCAACAGCATCGATGATATTAATCTGTAACATTTTACATCCGATCAATCTTCAATTC 486
Qy 181 CTCTACGGGTTCTGTTTGTATTTAGGCATTTTGGAAACGGCGGTACTATGGCGGTG 240
Db 487 CTCTACGGGTTCTGTTTGTATTTAGGCATTTTGGAAACGGCGGTACTATGGCGGTG 546
Qy 241 GCGAGAAACAGCGGCTCAATCGGCTCGCAACGTAATTTCTGCTCAAATCTTGATCTTACC 300
Db 547 GCGAGAAACAGCGGCTCAATCGGCTCGCAACGTAATTTCTGCTCAAATCTTGATCTTACC 606
Qy 301 GATTTGATATTGGTGTTCACAGCGAATCCAGTCACACCATGTCAGCGATGACCAAGAC 360
Db 607 GATTTGATATTGGTGTTCACAGCGAATCCAGTCACACCATGTCAGCGATGACCAAGAC 666
Qy 361 TGGGCATTCGGGTCAAGTGTGCAATTTAGTTCCTTTTGTCAAAATCGTGTGGTGT 420
Db 667 TGGGCATTCGGGTCAAGTGTGCAATTTAGTTCCTTTTGTCAAAATCGTGTGGTGT 726
Qy 421 GTGACGAGTTGGAGCTCATCTGCAATCTCTTAGATAAATTTCTGCATATCAACGATCCC 480
Db 727 GTGACGAGTTGGAGCTCATCTGCAATCTCTTAGATAAATTTCTGCATATCAACGATCCC 786
Qy 481 ACCAAACACAGGTTTCTATTGTCAGCGGTTTGGCAATAACATTTCTTATCTGGATGTC 540
Db 787 ACCAAACACAGGTTTCTATTGTCAGCGGTTTGGCAATAACATTTCTTATCTGGATGTC 846
Qy 541 TCACACTGATAAATCTACCGTATCTTATGTCCTTTTCGAGCAGTCGATGGAAGCTTTTAC 600
Db 847 TCACACTGATAAATCTACCGTATCTTATGTCCTTTTCGAGCAGTCGATGGAAGCTTTTAC 906
Qy 601 GTTCAGCCGGAGAACTCCATACTGCGGGGCACTTTTGGAGCAGGCGAAATGGCAGAGC 660
Db 907 GTTCAGCCGGAGAACTCCATACTGCGGGGCACTTTTGGAGCAGGCGAAATGGCAGAGC 966
Qy 661 GAAATAGTCGAAAGATTTACGGTTATGTTGTTACAGTTCGTGTCGGATG 720
Db 967 GAAATAGTCGAAAGATTTACGGTTATGTTGTTACAGTTCGTGTCGGATG 1026
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QY 287 ACTTGATCTTACCGATTGATATTGGTGTTCACAGCGATTCCAGTCCACACCCATGGTACG 346  
Db 206 CTTTGTGAGTTCTGACATTTTGTGGCGATTGTTAGTGGTTCACTAAGCCCGATACCG 265  
QY 347 CGATGACCAAGACTGGGCATTCGGGTCACTGATGTGCCATTTAGTTCCCTTTGTCAAATT 406  
Db 266 CATTCTAAGTTTGGTATTGGTGGACCATTTGTCAATTACTACCTTTGTTACAGG 325  
QY 407 CGTGTTCGGTGTGTGACGAGTTGGAGCTCTACTGCAATCTCCTTAGATAAAATTTCTGC 466  
Db 326 GTACCGCGTTGAGTTTTCACGTTTACCGCTTACCGCAATTGCAATTGACAGATATATTC 385  
QY 467 ATATCAACGATCCACCAACACCACTTCTATTCTGTCAGCGTTGGCGAATTAACATTTC 526  
Db 386 TCATCTGTCTACCGAAGAACCGGATACGAAAGATCAAGCAATGAAATGATAAGTT 445  
QY 527 TTATCTGGATGTCTCAACACTGATTAATCTACCGTATCTTTATG 570  
Db 446 TCAACAGCGCCATCTCAGTTGGGCTTTCCGTACCAATATTTCATG 489

## RESULT 6

US-10-650-467-15  
; Sequence 15, Application US/10650467  
; Publication No. US20050176069A1  
; GENERAL INFORMATION:  
; APPLICANT: Lowery, David E.  
; APPLICANT: Geary, Timothy G.  
; APPLICANT: Kubiak, Teresa M.  
; APPLICANT: Larsen, Martha J.  
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 28341/6223  
; CURRENT APPLICATION NUMBER: US/10/650,467  
; PRIOR FILING DATE: 2003-08-28  
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870  
; PRIOR FILING DATE: CURRENT FILING DATE: 2000-11-24  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 1352  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1350)  
; FEATURE:  
; OTHER INFORMATION: Clone identifier: CEGPCR14  
US-10-650-467-15

Query Match 6.8%; Score 78.8; DB 9; Length 1352;  
Best Local Similarity 47.4%; Pred. No. 7.4e-13;  
Matches 381; Conservative 0; Mismatches 402; Indels 21; Gaps 4;  
QY 134 TCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCATCTCTCTACGGGTTC 193  
Db 56 TCATGATTGGACAGTCCTCTTGAAGTTCCGCTGGATATTCAGTACTATATCTCTCA 115  
QY 194 TGTGTTGATTAGGCATTTTGAACGCGCGCTACTATGGCGGTGGCGAGAAACAAGC 253  
Db 116 TATTAATAATCCGATTGGTGGAAATGGGCTATTGATCACTTCAATTTAATCCGAAGA 175  
QY 254 GGTCCAAATCCGTCGACAGTATTCTGCTCAACTGTGATCTTCACCGATTGATATGG 313  
Db 176 AACTTTCCGTGGC---AAACATATTCTTGATAAACCTGCGCAGTTCTCGATTGCTCTTT 232  
QY 314 TGTTCACAGCATTCACAGTCACACCATGGTACCGATGACCAAGACTGGCATTCGGGT 373  
Db 233 GCATACGGCGGTGCGATCACTCCAGTATTCGCGTTTATGAGCGATGATATTTGGA 292  
QY 374 CAGTGTATGCCATTTAGTTCTCTTGTCAAAATCGGTGTTTGTGACGAGTTGGA 433  
Db 293 TAATTATGTAAATGGTTCGAACCTGTGACGGGTTTTCGGTGTCTCAATTTCTCATGT 352

QY 434 GCCTCACTGCAATCTCTCTTAGATAAAATTTCTGCATATCAACGATCCCAACCAACACCG 493  
Db 353 CTTTGTGTTACATCGCAATTGATAGATATCGAAGTATTGTGACGCCCACTCCGGGAACCAT 412  
QY 494 TTCTTATTGTCGTCAGCGTTGGCAATTAACATTTCTTATCTGGATAGTCTCAACACTGATA 553  
Db 413 GGTCTGATAGGCATGCAAGGTGGCTTCTGATGTTCATGCGGTGGTGGCTTCTCTTGCTA 472  
QY 554 ATCTACCGTATCTTATGTCTCTTCGAGCAGCTCGATGGAAGCTTTTACGTTTCAGCCCGGAG 613  
Db 473 GT-----TATCCTCTATATTACTCACAGAACTTTGAAACAATGGTTATTGA-----AA 520  
QY 614 AATCTCATACTCGGGGCACTTTTGGCAGAGCGGAAATTTGGCAGAGGAAATATGTCGAA 673  
Db 521 ATGTGACATTTATGTGAGAAATTTTTCGGCGAGTTCAATTTGGCAGTCGGATGAAATATCCA 580  
QY 674 AGATTTACGGAACCTACGGTTATGTCTTACAGTTCTGTCGCCGATGGCAGTGCATCACGT 733  
Db 581 AGTTGACATATATCTACGAGTTTATGATTTATTCAGCTGATTTATCCAGCAATTTATCATGT 640  
QY 734 ATTGCTACTCAAAATCTTTGCAAAAAGTGTCAAAAGACATGATCATCCAAAATGCTCAAT 793  
Db 641 CTTTGTGTTTATTATGATTTCTACAAAAGGTACAAACCGACTGGCTTGTGCGACGAGGAT 700  
QY 794 TCTGTCATCACTGACACAAAAGCAGAGAGTATCGCAGCTCCAGAAAGAAAGTGA 853  
Db 701 CCATGTTGACTGCGGCACACACAGGCTCAAAACAGCAG-----TTCGAAAGCGCAGTGA 754  
QY 854 ATTATATTCTAAATGCAATGGTTGTCAACATTTATCGGTGTTGGTTCCTTTAAACATTAC 913  
Db 755 TGTACGTGTGATTTCTAATGGTTATTGTTTTTATGGCTTGTCTGGTTCCTCGGCTTGTCCGCCG 814  
QY 914 TCAATTTGCTCAAGATTTTAAAA 937  
Db 815 TGAATTTGTCAGAGATCTCGNA 838

## RESULT 7

US-10-650-467-25  
; Sequence 25, Application US/10650467  
; Publication No. US20050176069A1  
; GENERAL INFORMATION:  
; APPLICANT: Lowery, David E.  
; APPLICANT: Geary, Timothy G.  
; APPLICANT: Kubiak, Teresa M.  
; APPLICANT: Larsen, Martha J.  
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 28341/6223  
; CURRENT APPLICATION NUMBER: US/10/650,467  
; CURRENT FILING DATE: 2003-08-28  
; PRIOR FILING DATE: CURRENT APPLICATION NUMBER: US/09/721,870  
; PRIOR FILING DATE: CURRENT FILING DATE: 2000-11-24  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 1374  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1371)  
; FEATURE:  
; OTHER INFORMATION: Clone identifier: CEGPCR7  
US-10-650-467-25

Query Match 5.6%; Score 66.6; DB 9; Length 1374;  
Best Local Similarity 48.3%; Pred. No. 4.4e-09;  
Matches 186; Conservative 0; Mismatches 199; Indels 0; Gaps 0;  
QY 180 CCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTCGAAACGGCGGTACTATGGCGGT 239  
Db 93 CGTGACCTTTTCTCTTTTCTTGTGACTCTTGGAAATGTGACCTGATTTACGTAAC 152



Db 525 GATCATCTGGTCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTACATGTGCA 584  
QY 585 CGATGAAGCTTTTAC 600  
Db 585 AGAAGAAAAATATTAC 600

RESULT 10  
US-11-060-756-2491  
; Sequence 2491, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 2491  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-060-756-2491

Query Match 5.2%; Score 61.6; DB 10; Length 1400;  
Best Local Similarity 46.3%; Pred. No. 1.6e-07;  
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

QY 165 ATCAATCTTCACATTCCTCTACGGGTCCTGTTGTATATTAGGCAATTTTGGAAACGGCGG 224  
Db 3 AGCAATCTTCATTAATTTCTCTACTTTCTGATCTCTTTTGTGATGATGGAAATACTGT 62

QY 225 CGTACTATGGCGGTGGCGAGAAACAGCGGCTCCAATCGGCTCGCAACGATTTCTTCTGCT 284  
Db 63 GGTTCGCTTTATTTGTAATGAGGAACAAACATATGCACACAGTCACCTAATCTCTTCATCTT 122

QY 285 CAACCTTGATCTTCACCGATTTGATATTTGGTGTTCACAGGATTCAGTCACACCATGGTA 344  
Db 123 AAACCTGGCCATAAGTGATTTACTAGTTGGCATAATCTGATGCGCTTATAACACCTGCTGGA 182

QY 345 CGCGATGACCAAGACTGGGCATTCGGGTCAGTGATGTCGCAATTTAGTTCCTTTGTCAAA 404  
Db 183 CAATATATAGCAGGATGGCCATTTGGAAACAGATGTGCAAGATCAGTGGATTTGTTCCA 242

QY 405 TTCTGTTTGGGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAAATTTCT 464  
Db 243 GGGATAATCTGTCGAGCTTCACTTTAGTTAGTTGCAATTTGCTGTAGATAGTTCCA 302

QY 465 GCATATCAACGATCCCAACCAACCAACAGTTTCTATTCTGTCAGGTTTGGCAATTAACATT 524  
Db 303 GTGTGTTGTTCTACCCCTTTTAAACCAAGCTCACTATCAAGACAGCGTTTGTCAATTAT 362

QY 525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTTCGAGCACGT 584  
Db 363 GATCATCTGGGTCCTAGCCATCACCATTATGTCTCACTGCAAGTAATGTATCATGTGCA 422

QY 585 CGATGGAAGCTTTTAC 600  
Db 423 AGAAGAAAAATATTAC 438

RESULT 11  
US-11-060-756-6763  
; Sequence 6763, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug

; TITLE OF INVENTION: Target Genes  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 6763  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-060-756-6763

Query Match 5.2%; Score 61.6; DB 10; Length 1400;  
Best Local Similarity 46.3%; Pred. No. 1.6e-07;  
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

QY 165 ATCAATCTTCACATTCCTCTACGGGTCCTGTTGTATATTAGGCAATTTTGGAAACGGCGG 224  
Db 3 AGCAATCTTCATTAATTTCTCTACTTTCTGATCTCTTTTGTGATGATGGAAATACTGT 62

QY 225 CGTACTATGGCGGTGGCGAGAAACAGCGGCTCCAATCGGCTCGCAACGATTTCTTCTGCT 284  
Db 63 GGTTCGCTTTATTTGTAATGAGGAACAAACATATGCACACAGTCACCTAATCTCTTCATCTT 122

QY 285 CAACCTTGATCTTCACCGATTTGATATTTGGTGTTCACAGGATTCAGTCACACCATGGTA 344  
Db 123 AAACCTGGCCATAAGTGATTTACTAGTTGGCATAATCTGATGCGCTTATAACACCTGCTGGA 182

QY 345 CGCGATGACCAAGACTGGGCATTCGGGTCAGTGATGTCGCAATTTAGTTCCTTTGTCAAA 404  
Db 183 CAATATATAGCAGGATGGCCATTTGGAAACAGATGTGCAAGATCAGTGGATTTGTTCCA 242

QY 405 TTCTGTTTGGGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAAATTTCT 464  
Db 243 GGGATAATCTGTCGAGCTTCACTTTAGTTAGTTGCAATTTGCTGTAGATAGTTCCA 302

QY 465 GCATATCAACGATCCCAACCAACCAACAGTTTCTATTCTGTCAGGTTTGGCAATTAACATT 524  
Db 303 GTGTGTTGTTCTACCCCTTTTAAACCAAGCTCACTATCAAGACAGCGTTTGTCAATTAT 362

QY 525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTTCGAGCACGT 584  
Db 363 GATCATCTGGGTCCTAGCCATCACCATTATGTCTCACTGCAAGTAATGTATCATGTGCA 422

QY 585 CGATGGAAGCTTTTAC 600  
Db 423 AGAAGAAAAATATTAC 438

RESULT 12  
US-10-060-369-8  
; Sequence 8, Application US/10060369  
; Publication No. US20030139589A1  
; GENERAL INFORMATION:  
; APPLICANT: Zastawny, Roman  
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR A4  
; FILE REFERENCE: 2931-104  
; CURRENT APPLICATION NUMBER: US/10/060,369  
; CURRENT FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 09/173565  
; PRIOR FILING DATE: 1998-08-16  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 8  
; LENGTH: 1440  
; TYPE: DNA  
; ORGANISM: Human  
US-10-060-369-8

Query Match 5.2%; Score 61.6; DB 6; Length 1440;  
Best Local Similarity 46.3%; Pred. No. 1.6e-07;  
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

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QY 165 ATCAATCTTCACATTCCTCTACGGGTTCTGTGTTATTTAGGCATTTTGGAAACGGCG 224
Db 255 AGCAATCTTCATTTATTTCTCTACTTTCTGATCTTCTTTTGTGCATGATGGGAAATACTGT 314
QY 225 CGTACTATGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTTATTTCTGCT 284
Db 315 GGTTCCTTTATTTGTAAGAGGAAACAACATATGCAACAGTCACTAATCTCTTCATCTT 374
QY 285 CAATCTGATCTTCACCGATTTGATTTGTTGTTTCAACGGATTCAGTCAACACATGGTA 344
Db 375 AAACCTGCCATAGTGAATTTACTAGTTGGCATATTTCTGCATGCTATATAACACATGCTGA 434
QY 345 CGCGATGACCAAGACTGGGCAATTCGGGTGAGTGGGCAATTTAGTTCTTCTTGTCAA 404
Db 435 CAATATTTATGAGGATGGCAATTTGGAAACAACGATGTGCAAGATCAAGTGAATGGTCCA 494
QY 405 TCGTGTTTCGGTGTGTTGAGAGTTGGAGCTCTCACTGCAATCTCTTTAGATAAATTTCT 464
Db 495 GGGATATCTCTGCGAGCTTCAGTCTTTTACGTTAGTTGCAATTCGTGTAGATAGTTCCA 554
QY 465 GCATATCAACGATCCCAACAAACACAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524
Db 555 GTGTGCTGTACCTCTTTTAAACCAAGCTCACTATCAAGACAGGTTTGTCAATTTAT 614
QY 525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTTCGAGCAGT 584
Db 615 GATCATCTGGGTCTTAGGCATCACCAATATGTCTCTCATGCAATGTTTACATGTGCA 674
QY 585 CGATGGAAGCTTTTAC 600
Db 675 AGAAGAAAATATTATAC 690
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RESULT 13
US-10-507-617-4
; Sequence 4, Application US/10507617
; Publication No. US20050119206A1
; GENERAL INFORMATION:
; APPLICANT: Eulenber, Karsten
; APPLICANT: Steuernagel, Arnd
; APPLICANT: Haeder, Thomas
; APPLICANT: Broenner, Guenter
; TITLE OF INVENTION: CG8327, CG10823, CG18418, CG15862, CG3768, CG11447 and CG16750
; TITLE OF INVENTION: Homologous Proteins Involved in the Regulation of Energy
; FILE REFERENCE: 2923-651
; CURRENT APPLICATION NUMBER: US/10/507,617
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: PCT/EP03/02714
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: EP 02 005 882.2
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: EP 002 006 012.5
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: EP 02 006 271.7
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: EP 02 006 810.2
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-507-617-4
Query Match 5.2%; Score 61.6; DB 9; Length 1560;
Best Local Similarity 46.3%; Pred. No. 1.7e-07;
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;
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QY 165 ATCAATCTTCACATTCCTCTACGGGTTCTGTGTTATTTAGGCATTTTGGAAACGGCG 224
Db 182 AGCAATCTTCATTTATTTCTCTACTTTCTGATCTTCTTTTGTGCATGATGGGAAATACTGT 241
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QY 225 CGTACTATGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTTATTTCTGCT 284
Db 242 GGTTCCTTTATTTGTAATAGGAAACAACATATGCAACAGTCACTAATCTCTTCATCTT 301
QY 285 CAATCTGATCTTCACCGATTTGATTTGTTTTCACAGCGATTCAGTCAACACATGGTA 344
Db 302 AAACCTGCCATAGTGAATTTACTAGTTGGCATATTTCTGCATGCTATATAACACATGCTGA 361
QY 345 CGCGATGACCAAGACTGGGCAATTCGGGTGAGTGGGCAATTTAGTTCTTCTTGTCAA 404
Db 362 CAATATTTATAGCAGATGGCCATTTGGAAACAACGATGTGCAAGATCAAGTGAATGGTCCA 421
QY 405 TCGTGTTTCGGTGTGTTGAGAGTTGGAGCTCTCACTGCAATCTCTTTAGATAAATTTCT 464
Db 422 GGGATATCTCTGCGAGCTTCAGTCTTTTACGTTAGTTGCAATTCGTGTAGATAGTTCCA 481
QY 465 GCATATCAACGATCCCAACCAACAGTTTCTTATTCGTCAAGCGTTGGCAATAACATT 524
Db 482 GTGTGCTGTCTACCTCTTTTAAACCAAGCTCACTATCAAGACAGGTTTGTCAATTTAT 541
QY 525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTTCGAGCAGT 584
Db 542 GATCATCTGGGTCTTAGGCATCACCAATATGTCTCTCATGCAATGTTTACATGTGCA 601
QY 585 CGATGGAAGCTTTTAC 600
Db 602 AGAAGAAAATATTATAC 617
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RESULT 14
US-10-949-140-1
; Sequence 1, Application US/10949140
; Publication No. US2005013644A1
; GENERAL INFORMATION:
; APPLICANT: Scully, Audra L.
; APPLICANT: Davis, Robert E.
; APPLICANT: Vanover, Kimberly E.
; APPLICANT: Gardell, Luis Roberto
; APPLICANT: Lamah, Jelvah
; APPLICANT: Kelly, Nicholas Michael
; APPLICANT: Bertozzi, Fabio
; TITLE OF INVENTION: TREATING NEUROPATHIC PAIN WITH
; TITLE OF INVENTION: NEUROPEPTIDE PF RECEPTOR 2 AGONISTS
; FILE REFERENCE: ACADIA.038A
; CURRENT APPLICATION NUMBER: US/10/949,140
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: 60/508,008
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: 60/506,130
; PRIOR FILING DATE: 2003-09-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-949-140-1
Query Match 5.2%; Score 61.6; DB 9; Length 1560;
Best Local Similarity 46.3%; Pred. No. 1.7e-07;
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;
```

```
QY 165 ATCAATCTTCACATTCCTCTACGGGTTCTGTGTTATTTAGGCATTTTGGAAACGGCG 224
Db 182 AGCAATCTTCATTTATTTCTCTACTTTCTGATCTTCTTTTGTGCATGATGGGAAATACTGT 241
QY 225 CGTACTATGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTTATTTCTGCT 284
Db 242 GGTTCCTTTATTTGTAATAGGAAACAACATATGCAACAGTCACTAATCTCTTCATCTT 301
QY 285 CAATCTGATCTTCACCGATTTGATTTGTTTTCACAGCGATTCAGTCAACACATGGTA 344
```



Db 302 ABACTGGCCATAAGTGAATTTACTAGTTGGCATATTTCTGTCATGCCTATAA CACTGTGGA 361  
Qy 345 CGCGATGACCAAGACTGGGCATTCGGGT CAGTGATGTGCCATTTAGTTCCTTTGTCAA 404  
Db 362 CAATATATTATAGCAGGATGGCCATTTGGAAACACGATGTGCAAGATCAGTGGATTGGTCCA 421  
Qy 405 TTCGTGTTGGTGTGTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCT 464  
Db 422 GGGAAATATCTGTCGAGCTTCAGTCTTTACGTTAGTTGCAATTTGCTGATAGGTGCTCA 481  
Qy 465 GCATATCAACGATGCCACCAAAACACAGTTTCTATTCTGTCAGCGTTGGCAATAACATT 524  
Db 482 GTGTGTGGTCTACCCCTTTTAAACCAAAAGCTCACTATCAAGACAGCGTTTGTCAATTATTAT 541  
Qy 525 TCTTATCTGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTTCGAGCAGCT 584  
Db 542 GATCATCTGGTCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTTACATGTGCA 601  
Qy 585 CGATGGAAGCTTTTAC 600  
Db 602 AGAAGAAAAAATATTAC 617

## RESULT 15

US-10-276-774-743  
; Sequence 743, Application US/10276774  
; Publication No. US20040053245A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-030  
; CURRENT APPLICATION NUMBER: US/10/276, 774  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/560,875  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 09/496,914  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 2700  
; SOFTWARE: Custom  
; SEQ ID NO 743  
; LENGTH: 1824  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-276-774-743

Query Match 5.2%; Score 61.6; DB 7; Length 1824;  
Best Local Similarity 46.3%; Pred. No. 1.9e-07;  
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

Qy 165 ATCAATCTTCACATTCCTCTACGGGTTCCCTGTTGTTGTTATTTAGGCATTTTGGAAACGGCG 224  
Db 441 AGCAATCTTCATTAATTTCTCTACTTTCTGATCTCTTTTGTGTCATGATGGAAATACTGT 500  
Qy 225 CGTACTATGGCGGTGGCGGAAACAGCGGTCCCAATCGGCTCGCAAGTATTTCTGCT 284  
Db 501 GGTTCGCTTATTGTTAATGAGGAACAAACATATGCACAGTCACTAAATCTCTTCATCTT 560  
Qy 285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCAGTCCAGTCACACCATTGTA 344  
Db 561 AAACCTGGCCATAAGTGAATTTACTAGTTGGCATATTCTGCATGCCCTATAACACTGCTGGA 620  
Qy 345 CGCGATGACCAAGACTGGGCATTCGGGT CAGTGATGTGCCATTTAGTTTCCTTTGTCAA 404  
Db 621 CAATATTATAGCAGGATGCCATTTGGAAACACGATGTGCAAGATCAGTGGATTGGTCCA 680  
Qy 405 TTCGTGTTCCGTGTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCT 464  
Db 681 GGGAAATATCTGTCGAGCTTCAGTCTTTTACGTTAGTTGCAATTTGCTGTAGATAGGTCCA 740  
Qy 465 GCATATCAACGATCCCAACAAACACAGTTTCTATTCTCAAGCGTTGCAATTAACATT 524  
Db 741 GTGTGTGGTCTACCCCTTTTAAACCAAGCTCACTATCAAGACAGCGTTTGTCAATTATTAT 800

Qy 525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTTCTTTTCGAGCAGCT 584  
Db 801 GATCATCTGGTCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTTACATGTGCA 860  
Qy 585 CGATGGAAGCTTTTAC 600  
Db 861 AGAAGAAAAAATATTAC 876

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Job time : 1121 secs



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				19: /SID55/ptodata/2/pubpna/US60_NEW_PUB.seq:*			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	62.2	5.2	2025	17	US-11-136-527-2424
2	61.6	5.2	1302	10	US-10-992-577-5
3	61.6	5.2	1936	10	US-10-510-018-1
4	57.8	4.8	1605	18	US-11-183-615-3
5	57.8	4.8	1888	17	US-11-080-991-25
6	57.8	4.8	2752	13	US-10-960-414-9
7	53.4	4.5	1329	18	US-11-100-640-33
8	53.4	4.5	1578	9	US-10-473-173-20
9	50	4.2	1299	18	US-11-223-294-38
10	50	4.2	1410	10	US-10-992-577-1
11	48.8	4.1	3219	17	US-11-136-527-4059
12	48.8	4.1	3219	18	US-11-224-663-594
13	48.8	4.1	3219	18	US-11-224-525-594
14	48.8	4.1	3295	17	US-11-136-527-3736

15	47.6	4.0	1147	17	US-11-136-527-2750	Sequence 2750, Ap
16	47.4	4.0	1254	17	US-11-136-527-2754	Sequence 2754, Ap
17	47.4	4.0	1334	10	US-10-992-577-43	Sequence 43, Appl
18	47.4	4.0	2471	17	US-11-136-527-2231	Sequence 2231, Ap
19	47.2	4.0	1450	17	US-11-136-527-3841	Sequence 3841, Ap
20	47.2	4.0	1450	18	US-11-036-196-1852	Sequence 1852, Ap
21	47	3.9	1560	17	US-11-136-527-3742	Sequence 3742, Ap
22	47	3.9	1865	10	US-10-533-355-9	Sequence 9, Appli
23	46.6	3.9	1069	18	US-11-183-615-5	Sequence 5, Appli
24	46.6	3.9	1201	18	US-11-183-615-16	Sequence 16, Appl
25	46.6	3.9	1365	11	US-10-987-856-14	Sequence 14, Appl
26	46.6	3.9	1406	18	US-11-183-615-6	Sequence 6, Appli
27	46.6	3.9	1457	11	US-10-987-856-3	Sequence 3, Appli
28	46.6	3.9	1500	18	US-11-183-615-12	Sequence 12, Appl
29	45.4	3.8	1211	13	US-10-960-414-430	Sequence 430, App
30	45.4	3.8	1452	17	US-11-136-527-3122	Sequence 3122, Ap
31	45.2	3.8	1290	17	US-11-136-527-2457	Sequence 2457, Ap
32	45.2	3.8	1290	17	US-11-136-527-6553	Sequence 6553, Ap
33	45	3.8	3288	17	US-11-136-527-3178	Sequence 3178, Ap
34	44.8	3.8	1290	18	US-11-223-294-56	Sequence 56, Appl
35	44.2	3.7	1002	17	US-11-127-877-20	Sequence 20, Appl
36	44.2	3.7	1677	18	US-11-262-284-33	Sequence 33, Appl
37	44	3.7	1339	17	US-11-136-527-4061	Sequence 4061, Ap
38	44	3.7	1339	18	US-11-224-663-596	Sequence 596, App
39	44	3.7	1339	18	US-11-224-525-596	Sequence 596, App
40	44	3.7	2580	17	US-11-136-527-3525	Sequence 3525, Ap
41	43.4	3.6	1504	17	US-11-136-527-3501	Sequence 3501, Ap
42	43.4	3.6	2422	17	US-11-136-527-2272	Sequence 2272, Ap
43	43.2	3.6	1290	18	US-11-223-294-55	Sequence 55, Appl
44	43.2	3.6	1293	10	US-10-992-577-7	Sequence 7, Appli
45	43.2	3.6	1293	11	US-10-508-892-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-11-136-527-2424  
; Sequence 2424, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2424  
; LENGTH: 2025  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-2424

Query Match		5.2%	Score 62.2;	DB 17;	Length 2025;
Best Local Similarity		50.5%;	Pred. No. 5e-07;		
Matches 151;		Conservative 0;	Mismatches 148;	Indels 0;	Gaps 0;
QY	165	ATCAATCTTCACATTCCTCTACGGGTTCTGTTTGTATTAGGCATTTTGGAAACGGCGG	224		
Db	554	ATACATCAACAGATTGTATCATGCTCGTGTGTCTAGGCATCATCGGAACCTCCAC	613		
QY	225	CGTACTATGGGGTGGCGAGAACAGGGGCTCCAACTGGCTCCAGCTATTTCTGT	284		
Db	614	ACTGTAGAATCATCTACAAGAACAGTCAGTAATGTCCTCAATATCTTGTATC	673		
QY	285	CAACTTGTATCTTCACCGATTTTCATATTGTTGTTCACAGGATTCAGTCACACACCTGGTA	344		
Db	674	CAGCTGGCTCTGGGAGATCTCTACATCATCATCTCGACATTCCTCAATTAATGCTACAA	733		

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QY 345 CGCGATGACCAAGACTGGGCAATTCGGGTCTAGTGATGGCCATTTAGTTCTTTGTCTCAA 404
Db 734 GCTGCTGGCAGGGGACTGGCCATTTGGAGCTGAGATGTGCAAGCTGGTGGCCSTTCATACA 793
QY 405 TTCTGTTTGGTGTGTTGTGACGAGTTGGAGCCTCACTGCAATCTCTTTAGATAAATTTTC 463
Db 794 GAAAGCTTCTGTGGGATCACAGTGTCTGAGTCTATGTCTTAAGTATTGACAGATATC 852

RESULT 2
US-10-992-577-5
; Sequence 5, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; FILE REFERENCE: 57155-D/JFW
; CURRENT APPLICATION NUMBER: US/10/992,577
; CURRENT FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1302
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-992-577-5

Query Match 5.2%; Score 61.6; DB 10; Length 1302;
Best Local Similarity 46.3%; Pred. No. 6.4e-07;
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

QY 165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTGTATAGGCATTTTGGAAACGGGG 224
Db 165 AGCAATCTTCATATTTCTACTTCTCTGATCTCTTTTGTGTCATGATGGGAAATACTGT 224
QY 225 CGTACTATGGGCGGTGGGAGAAACAAGCGGCTCCAAATCGGCTCGCAACGTATTTCTGCT 284
Db 225 GGTTCGTTTATGTAATGAGGAACAACATATGCACAGTCACTAATCTCTTCATCTT 284
QY 285 CAACTTGATCTTCACCGATTTGATATGTTGTTCACAGCGATTCAGTCACACCATGGTA 344
Db 285 AAACCTGGCCATAAGTATTTACTAGTTGGCATATTTCTGCATGCTATAACACTGCTGA 344
QY 345 CGCGATGACCAAGACTGGGCAATTCGGGTCTAGTGATGGCCATTTAGTTCCTTTGTCAA 404
Db 345 CAAATATTATAGCAGGATGGCCATTTGGAAACAACGATGTGCAAGATCAGTGGATTTGTTCCA 404
QY 405 TTCTGTTTGGTGTGTTGTGACGAGTTGGAGCCTCACTGCAATCTCTCTAGATAAATTTCT 464
Db 405 GGGATAATCTGTCGAGCTTCTAGTCTTTACGTTAGTTGGCAATTTGCTAGATAGTTCCA 464
QY 465 GCATATCAACGATCCCAACCAACCAACAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524
Db 465 GTGTGTGGTCTACCCCTTTTAAACCAAGCTCACTATCAAGACAGCGTTTGTCAATTAT 524
QY 525 TCTTATCTGGATAGTCTCAACTGATTAATCTACCGTATCTTATGCTTTTGGACACGT 584
Db 525 GATCATCTGGGCTCTAGCCATCCCATTTATGTTCTCCATCTGCAGTAATGTTACATGTGCA 584
QY 585 CGATGGAAGCTTTTAC 600
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Db 585 AGAAGAAAATATTATAC 600

RESULT 3
US-10-510-018-1
; Sequence 1, Application US/10510018
; Publication No. US20050244896A1
; GENERAL INFORMATION:
; APPLICANT: Golz, Stefan
; APPLICANT: Bruggemeyer, Ulf
; APPLICANT: Weingarten, Bernhard
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
; TITLE OF INVENTION: Neuropeptide FF Receptor 2 (NPFF2)
; FILE REFERENCE: Le A 35 945
; CURRENT APPLICATION NUMBER: US/10/510,018
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: PCT/EP2003/002962
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: EP 02007270.8
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1
; LENGTH: 1936
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-510-018-1

Query Match 5.2%; Score 61.6; DB 10; Length 1936;
Best Local Similarity 46.3%; Pred. No. 7.3e-07;
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

QY 165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTGTATAGGCATTTTGGAAACGGGG 224
Db 539 AGCAATCTTCATATTTCTACTTCTCTGATCTCTTTTGTGTCATGATGGGAAATACTGT 598
QY 225 CGTACTATGGGCGGTGGGAGAAACAAGCGGCTCCAAATCGGCTCGCAACGTATTTCTGCT 284
Db 599 GGTTCGTTTATGTAATGAGGAACAACATATGCACAGTCACTAATCTCTTCATCTT 658
QY 285 CAACTTGATCTTCACCGATTTGATATGTTGTTCACAGCGATTCAGTCACACCATGGTA 344
Db 659 AAACCTGGCCATAAGTATTTACTAGTTGGCATATTTCTGCATGCTATAACACTGCTGA 718
QY 345 CGCGATGACCAAGACTGGGCAATTCGGGTCTAGTGATGGCCATTTAGTTCCTTTGTCAA 404
Db 719 CAAATATTATAGCAGGATGGCCATTTGGAAACAACGATGTGCAAGATCAGTGGATTTGTTCCA 778
QY 405 TTCTGTTTGGTGTGTTGTGACGAGTTGGAGCCTCACTGCAATCTCTCTAGATAAATTTCT 464
Db 779 GGGATAATCTGTCGAGCTTCTAGTCTTTTACGTTAGTTGCAATTTGCTAGATAGTTCCA 838
QY 465 GCATATCAACGATCCCAACCAACCAACAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524
Db 839 GTGTGTGGTCTACCCCTTTTAAACCAAGCTCACTATCAAGACAGCGTTTGTCAATTAT 898
QY 525 TCTTATCTGGATAGTCTCAACTGATTAATCTACCGTATCTTATGCTTTTGGACACGT 584
Db 899 GATCATCTGGGCTCTAGCCATCCCATTTATGTTCTCCATCTGCAGTAATGTTACATGTGCA 958
QY 585 CGATGGAAGCTTTTAC 600
Db 959 AGAAGAAAATATTATAC 974

RESULT 4
US-11-183-615-3
; Sequence 3, Application US/11183615
; Publication No. US20060040964A1
; GENERAL INFORMATION:
; APPLICANT: Bakthavatchalam, Rajagopal
; APPLICANT: Blum, Charles A.
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; APPLICANT: Brielmann, Harry L.
; APPLICANT: Darrow, James W.
; APPLICANT: De Lombaert, Stephane W.
; APPLICANT: Hutchinson, Alan W.
; APPLICANT: Tran, Jennifer W.
; APPLICANT: Zheng, Xiaozhang W.
; APPLICANT: Elliott, Richard L.
; APPLICANT: Hammond, Marlys L.
; TITLE OF INVENTION: SPIRO[ISOBIENZOPURAN-1,4'-PIPERIDIN]-3-ONES AND
; TITLE OF INVENTION: 3H-SPIROBIENZOPURAN-1,4'-PIPERIDINES
; FILE REFERENCE: U 014539-7
; CURRENT APPLICATION NUMBER: US/11/183,615
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/410,648
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: 10/013,846
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 60/254,990
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-183-615-3

Query Match      4.8%; Score 57.8; DB 18; Length 1605;
Best Local Similarity 46.4%; Pred. No. 8.4e-06;
Matches 188; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

QY 75 AAGTCATTCCGAACAATGGCTCGTGCAATTCAGATCGCTGAGGCGAATTCGGCGCAACAGGCAT 134
Db 226 AAATCAATTCAGTCCACTCTAAATTTCTCAGAGAAGAAATGCCAGCTTCTGGCTTTTGAAAA 285
QY 135 CGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCTCT 194
Db 286 TGATGATTGTCATCTGCCCTTGCCCATGATATTACCTTAGCTCTTGCTTTATGGAGCTGT 345
QY 195 GTTTGTAATTAGGCATTTTGGAAACGGCGCGCTACTATGGCGGTGGCGAGAAACAAGCG 254
Db 346 GATCATTCTTGGTGTCTCTGGAAACCTGGCCCTTGATCATATAATCATCTTGAACAAAAGGA 405
QY 255 GCTCCAAATCGGTCGCAAGTATTCTGCTCAACTTGATCTTCACCGATTGATATTGGT 314
Db 406 GATGAGAAATGTTACCAACATCTCGAATGTGAACCTTTCTCTCAGACTTGTCTTGTTC 465
QY 315 GTTCACAGCGATTCACGATCACACCAATGTCACGATGACCAAGACTGGGCGATTCGGGTC 374
Db 466 CATCATGTCTCTCCCTTTACATTTGCTACATTAATGGACCACTGGGTCTTTGGTGA 525
QY 375 AGTGATGTGCCATTTAGTTCCCTTTGTCAAATTCGTTTCGGTGTTCGACGAGTTGGAG 434
Db 526 GCGCATGTGTAAGTTGAATCCCTTTGTGCAATGTGTTCAATCACTGTGTCCATTTTCTC 585
QY 435 CCTCACTGCAATCTCTTAGATAAATTTCTGCATATCAACGATCC 479
Db 586 TCTGGTTCTCATTTGTGTGGAAACGACATCAGCTGATTAATCAACCC 630

RESULT 5
US-11-080-991-25
; Sequence 25, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petter Ole
; APPLICANT: Veiby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
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; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1888
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1814, 1834, 1850
; OTHER INFORMATION: n = A,T,C or G
; US-11-080-991-25

Query Match      4.8%; Score 57.8; DB 17; Length 1888;
Best Local Similarity 46.4%; Pred. No. 8.9e-06;
Matches 188; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

QY 75 AAGTCATTCCGAACAATGGCTCGTGCAATTCAGATCGCTGAGGCGAATTCGGCGCAACAGGCAT 134
Db 498 AAATCAATTCAGTCCACTCTAAATTTCTCAGAGAAGAAATGCCAGCTTCTGGCTTTTGAAAA 557
QY 135 CGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCTCT 194
Db 558 TGATGATTGTCATCTGCCCTTGCCCATGATATTACCTTAGCTCTTGCTTTATGGAGCTGT 617
QY 195 GTTTGTAATTAGGCATTTTGGAAACGGCGCGCTACTATGGCGGTGGCGAGAAACAAGCG 254
Db 618 GATCATTCTTGGTGTCTCTGGAAACCTGGCCCTTGATCATATAATCATCTTGAACAAAAGGA 677
QY 255 GCTCCAAATCGGTCGCAAGTATTCTGCTCAACTTGATCTTCACCGATTGATATTGGT 314
Db 678 GATGAGAAATGTTACCAACATCTCGAATGTGAACCTTTCTCTCAGACTTGTCTTGTTC 737
QY 315 GTTCACAGCGATTCACGATCACACCAATGTCACGATGACCAAGACTGGGCGATTCGGGTC 374
Db 738 CATCATGTCTCTCCCTTTACATTTGCTACATTAATGGACCACTGGGTCTTTGGTGA 797
QY 375 AGTGATGTGCCATTTAGTTCCCTTTGTCAAATTCGTTTCGGTGTTCGACGAGTTGGAG 434
Db 798 GCGCATGTGTAAGTTGAATCCCTTTGTGCAATGTGTTCAATCACTGTGTCCATTTTCTC 857
QY 435 CCTCACTGCAATCTCTTAGATAAATTTCTGCATATCAACGATCC 479
Db 858 TCTGGTTCTCATTTGTGTGGAAACGACATCAGCTGATTAATCAACCC 902

RESULT 6
US-10-960-414-9
; Sequence 9, Application US/10960414
; Publication No. US20060074565A1
; GENERAL INFORMATION:
; APPLICANT: MILLER, LANCE D.
; APPLICANT: GEORGE, JOSH
; APPLICANT: VEGA, VINCENTUS B.
; TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,
; TITLE OF INVENTION: PROGNOSIS, AND DIAGNOSIS OF CANCERS
; FILE REFERENCE: 38271-76067
; CURRENT APPLICATION NUMBER: US/10/960,414
; CURRENT FILING DATE: 2004-10-06
; NUMBER OF SEQ ID NOS: 500
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-960-414-9

Query Match      4.8%; Score 57.8; DB 13; Length 2752;
Best Local Similarity 46.4%; Pred. No. 1e-05;
Matches 188; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

QY 75 AAGTCATTCCGAACAATGGCTCGTGCAATTCAGATCGCTGAGGCGAATTCGGCGCAACAGGCAT 134
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US-11-224-663-594  
; Sequence 594, Application US/11224663  
; Publication No. US20060078921A1  
; GENERAL INFORMATION:  
; APPLICANT: BOESS, FRANZISKA  
; APPLICANT: SUTER-DICK, LAURA  
; APPLICANT: WOLF, DETLEF  
; TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY  
; FILE REFERENCE: 21199 US2  
; CURRENT APPLICATION NUMBER: US/11/224,663  
; PRIOR FILING DATE: 2005-09-12  
; PRIOR APPLICATION NUMBER: 10/388,934  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: EP 02005336.9  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: EP 02015657.6  
; PRIOR FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 862  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 594  
; LENGTH: 3219  
; TYPE: DNA  
; ORGANISM: Rattus rattus  
US-11-224-663-594

Query Match 4.1%; Score 48.8; DB 18; Length 3219;  
Best Local Similarity 51.4%; Pred. No. 0.004;  
Matches 113; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 152 ACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTCTCTGTTGTATTAGGCATTT 211  
DB 152 ACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTCTCTGTTGTATTAGGCATTT 211  
QY 212 TTGGAACGGCGGTACTATGCGGTGGCGAGAAACAAGCGGTCCCAATCGGCTCGCA 271  
DB 212 TTGGAACGGCGGTACTATGCGGTGGCGAGAAACAAGCGGTCCCAATCGGCTCGCA 271  
QY 272 ACATATTTCTGCTCAACTTGATCTTCACCGATTTGATATGGTGTTCACAGCGATTCCAG 331  
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QY 462 GCGTCTTCTCTCAATCTCGCTTGGCTGACTATGCTTTTGTGCTGACTTTGCCCTGT 521  
DB 462 GCGTCTTCTCTCAATCTCGCTTGGCTGACTATGCTTTTGTGCTGACTTTGCCCTGT 521  
QY 332 TCACACCATGGTACCGGATGACCAAGACTGGGCATTCGG 371  
DB 332 TCACACCATGGTACCGGATGACCAAGACTGGGCATTCGG 371  
QY 522 GGGCAGTCTATACCGCTATGGAGTACCGCTGGCCCTTCGG 561  
DB 522 GGGCAGTCTATACCGCTATGGAGTACCGCTGGCCCTTCGG 561

RESULT 13  
US-11-224-525-594  
; Sequence 594, Application US/11224525  
; Publication No. US20060084096A1  
; GENERAL INFORMATION:  
; APPLICANT: BOESS, FRANZISKA  
; APPLICANT: SUTER-DICK, LAURA  
; APPLICANT: WOLF, DETLEF  
; TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY  
; FILE REFERENCE: 21199 US1  
; CURRENT APPLICATION NUMBER: US/11/224,525  
; PRIOR FILING DATE: 2005-09-12  
; PRIOR APPLICATION NUMBER: 10/388,934  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: EP 02005336.9  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: EP 02015657.6  
; PRIOR FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 862  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 594  
; LENGTH: 3219  
; TYPE: DNA  
; ORGANISM: Rattus rattus  
US-11-224-525-594

Query Match 4.1%; Score 48.8; DB 18; Length 3219;

Best Local Similarity 51.4%; Pred. No. 0.004;  
Matches 113; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 152 ACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTCTCTGTTGTATTAGGCATTT 211  
DB 152 ACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTCTCTGTTGTATTAGGCATTT 211  
QY 212 TTGGAACGGCGGTACTATGCGGTGGCGAGAAACAAGCGGTCCCAATCGGCTCGCA 271  
DB 212 TTGGAACGGCGGTACTATGCGGTGGCGAGAAACAAGCGGTCCCAATCGGCTCGCA 271  
QY 272 ACATATTTCTGCTCAACTTGATCTTCACCGATTTGATATGGTGTTCACAGCGATTCCAG 331  
DB 272 ACATATTTCTGCTCAACTTGATCTTCACCGATTTGATATGGTGTTCACAGCGATTCCAG 331  
QY 462 GCGTCTTCTCTCAATCTCGCTTGGCTGACTATGCTTTTGTGCTGACTTTGCCCTGT 521  
DB 462 GCGTCTTCTCTCAATCTCGCTTGGCTGACTATGCTTTTGTGCTGACTTTGCCCTGT 521  
QY 332 TCACACCATGGTACCGGATGACCAAGACTGGGCATTCGG 371  
DB 332 TCACACCATGGTACCGGATGACCAAGACTGGGCATTCGG 371  
QY 522 GGGCAGTCTATACCGCTATGGAGTACCGCTGGCCCTTCGG 561  
DB 522 GGGCAGTCTATACCGCTATGGAGTACCGCTGGCCCTTCGG 561

RESULT 14  
US-11-136-527-3736  
; Sequence 3736, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3736  
; LENGTH: 3295  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-3736

Query Match 4.1%; Score 48.8; DB 17; Length 3295;  
Best Local Similarity 51.4%; Pred. No. 0.004;  
Matches 113; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 152 ACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTCTCTGTTGTATTAGGCATTT 211  
DB 152 ACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTCTCTGTTGTATTAGGCATTT 211  
QY 212 TTGGAACGGCGGTACTATGCGGTGGCGAGAAACAAGCGGTCCCAATCGGCTCGCA 271  
DB 212 TTGGAACGGCGGTACTATGCGGTGGCGAGAAACAAGCGGTCCCAATCGGCTCGCA 271  
QY 272 ACATATTTCTGCTCAACTTGATCTTCACCGATTTGATATGGTGTTCACAGCGATTCCAG 331  
DB 272 ACATATTTCTGCTCAACTTGATCTTCACCGATTTGATATGGTGTTCACAGCGATTCCAG 331  
QY 480 GCGTCTTCTCTCAATCTCGCTTGGCTGACTATGCTTTTGTGCTGACTTTGCCCTGT 539  
DB 480 GCGTCTTCTCTCAATCTCGCTTGGCTGACTATGCTTTTGTGCTGACTTTGCCCTGT 539  
QY 332 TCACACCATGGTACCGGATGACCAAGACTGGGCATTCGG 371  
DB 332 TCACACCATGGTACCGGATGACCAAGACTGGGCATTCGG 371  
QY 540 GGGCAGTCTATACCGCTATGGAGTACCGCTGGCCCTTCGG 579  
DB 540 GGGCAGTCTATACCGCTATGGAGTACCGCTGGCCCTTCGG 579

RESULT 15  
US-11-136-527-2750  
; Sequence 2750, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25



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Db 241 GCGGAGACAGCGCTCCATCGCTCGCAAGTATTTCTGCTCAACTTGATCTTCACC 300  
Qy 301 GATTGTGATTTGGTGTTCACAGCGATTCAGTCAACCATGGTACGCGATGACCAAGAC 360  
Db 301 GATTGTGATTTGGTGTTCACAGCGATTCAGTCAACCATGGTACGCGATGACCAAGAC 360  
Qy 361 TGGGCAATTCGGGTGATGATGCGATGATTTAGTTCCTTTGTCAAAATTCGGTGTGTTT 420  
Db 361 TGGGCAATTCGGGTGATGATGCGATGATTTAGTTCCTTTGTCAAAATTCGGTGTGTTT 420  
Qy 421 GTGACGAGTTGGAGCTCACTGCAATCTCTTTAGATAAATTTCTGCATATCAACGATCCC 480  
Db 421 GTGACGAGTTGGAGCTCACTGCAATCTCTTTAGATAAATTTCTGCATATCAACGATCCC 480  
Qy 481 ACCAAACAAACGATTTCTATTCGTCAAGCGTTGGCAATAAATTTCTTATCTGGATAGTC 540  
Db 481 ACCAAACAAACGATTTCTATTCGTCAAGCGTTGGCAATAAATTTCTTATCTGGATAGTC 540  
Qy 541 TCACACTGATATAATCTACCGTATCTTATGCTTTTTCGAGCAGTCCGATGGAGCTTTTAC 600  
Db 541 TCACACTGATATAATCTACCGTATCTTATGCTTTTTCGAGCAGTCCGATGGAGCTTTTAC 600  
Qy 601 GTTCAGCCCGGAGAACTCCATCTGCGGCACTTTTTCGAGCGAGCGCAATTTGGCAGAGC 660  
Db 601 GTTCAGCCCGGAGAACTCCATCTGCGGCACTTTTTCGAGCGAGCGCAATTTGGCAGAGC 660  
Qy 661 GAAATAGTCGAAAGATTTACGGAATACGCTTATGTTTACAGTTCTGTCGCGGATG 720  
Db 661 GAAATAGTCGAAAGATTTACGGAATACGCTTATGTTTACAGTTCTGTCGCGGATG 720  
Qy 721 GCAGTGATCAGTATGCTTCTCAAAATCTTGCAGAAAGTGTCAAAAGACATGATCATC 780  
Db 721 GCAGTGATCAGTATGCTTCTCAAAATCTTGCAGAAAGTGTCAAAAGACATGATCATC 780  
Qy 781 CAAATAGCTCAATCTGTCATCACTGACACAAAAGCAGAGAGTGTGCGACGTCACGA 840  
Db 781 CAAATAGCTCAATCTGTCATCACTGACACAAAAGCAGAGAGTGTGCGACGTCACGA 840  
Qy 841 AAGAAAGATGAAATATATTTCTAATGCAATGTTGTGTCACATTTATCGGGTGTGGTTG 900  
Db 841 AAGAAAGATGAAATATATTTCTAATGCAATGTTGTGTCACATTTATCGGGTGTGGTTG 900  
Qy 901 CTTTAAATCTACTCAATTTGCTCAAGATTTTAAAGAGCCGCAATGGCTAAACGT 960  
Db 901 CTTTAAATCTACTCAATTTGCTCAAGATTTTAAAGAGCCGCAATGGCTAAACGT 960  
Qy 961 CAGCGCTTCTTCGGGCAATTAATGCTCAGTCATAGCCATGCTCTTATGCTCTGGAAC 1020  
Db 961 CAGCGCTTCTTCGGGCAATTAATGCTCAGTCATAGCCATGCTCTTATGCTCTGGAAC 1020  
Qy 1021 CTTCTGCTATTTCTTTTGGCTGACAGAAAACAAAGAGCTTCGGAGCTGTCAAAAATATCTC 1080  
Db 1021 CTTCTGCTATTTCTTTTGGCTGACAGAAAACAAAGAGCTTCGGAGCTGTCAAAAATATCTC 1080  
Qy 1081 AACTCAACAGAGGTTTCGAAAAGAGCAGGTGTTCTGGAATTCGAGGAGTCCAGCTACAC 1140  
Db 1081 AACTCAACAGAGGTTTCGAAAAGAGCAGGTGTTCTGGAATTCGAGGAGTCCAGCTACAC 1140  
Qy 1141 GACCTCTCTCCGACCTCTACTCAATTCGGAACAGATGTCAGGCAACTCTTTTCTA 1193  
Db 1141 GACCTCTCTCCGACCTCTACTCAATTCGGAACAGATGTCAGGCAACTCTTTTCTA 1193

RESULT 2

US-09-721-870-39  
; Sequence 39, Application US/09721870  
; Patent No. 6632621  
; GENERAL INFORMATION:  
; APPLICANT: Lowery, David E.  
; APPLICANT: Geary, Timothy G.  
; APPLICANT: Kubiak, Teresa M.  
; APPLICANT: Larsen, Martha J.

; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 28341/6223  
; CURRENT APPLICATION NUMBER: US/09/721,870  
; CURRENT FILING DATE: 2000-11-24  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 39  
; LENGTH: 1500  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1497)  
; FEATURE:  
; OTHER INFORMATION: Clone identifier: CEGPCR19  
US-09-721-870-39

Query Match 100.0%; Score 1193; DB 3; Length 1500;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTTAGTTCGGCGGCCACCAATTCGACCAATTTCAACCAACAGACTCCCTCCACCATC 60  
Db 307 ATGGTTAGTTCGGCGGCCACCAATTCGACCAATTTCAACCAACAGACTCCCTCCACCATC 366  
Qy 61 AGCAACGTTATCACAGTCAATTCGAAACAATGGCTCGTCAATTCAGATCGCTGAGCGGATT 120  
Db 367 AGCAACGTTATCACAGTCAATTCGAAACAATGGCTCGTCAATTCAGATCGCTGAGCGGATT 426  
Qy 121 CGCGCACAAAGCATCGATGATATTAATCTGTAGATTTTATCATCCGATCAATCTTCACATTC 180  
Db 427 CGCGCACAAAGCATCGATGATATTAATCTGTAGATTTTATCATCCGATCAATCTTCACATTC 486  
Qy 181 CTCTACGGGTTCTGTTTGTATTAAGGCATTTTGGAAAAGCGCGGCTACTATGGCGGTG 240  
Db 487 CTCTACGGGTTCTGTTTGTATTAAGGCATTTTGGAAAAGCGCGGCTACTATGGCGGTG 546  
Qy 241 CGGAGAACAAAGCGCTCCAATCGCTCGCAACGATTTCTGCTCAACTTGATCTTCACC 300  
Db 547 CGGAGAACAAAGCGCTCCAATCGCTCGCAACGATTTCTGCTCAACTTGATCTTCACC 606  
Qy 301 GATTGTATTTGGTGTTCACAGCATTCAGTCAACCATGGTACGCGATGACCAAGAC 360  
Db 607 GATTGTATTTGGTGTTCACAGCATTCAGTCAACCATGGTACGCGATGACCAAGAC 666  
Qy 361 TGGGCAATTCGGGTGATGATGCGATTTAGTTCCTTTGTCAAAATTCGGTGTGGTGT 420  
Db 667 TGGGCAATTCGGGTGATGATGCGATTTAGTTCCTTTGTCAAAATTCGGTGTGGTGT 726  
Qy 421 GTGACGAGTTGGAGCTCACTGCAATCTCTTATGATAAATTTCTGCATATCAACGATCCC 480  
Db 727 GTGACGAGTTGGAGCTCACTGCAATCTCTTATGATAAATTTCTGCATATCAACGATCCC 786  
Qy 481 ACCAAACAAACGATTTCTATTCGTCAAGCGTTGGCAATAAATTTCTTATCTGGATAGTC 540  
Db 787 ACCAAACAAACGATTTCTATTCGTCAAGCGTTGGCAATAAATTTCTTATCTGGATAGTC 846  
Qy 541 TCACACTGATATAATCTACCGTATCTTATGCTTTTCGAGCAGTCCGATGGAGCTTTTAC 600  
Db 847 TCACACTGATATAATCTACCGTATCTTATGCTTTTCGAGCAGTCCGATGGAGCTTTTAC 906  
Qy 601 GTTCAGCCCGGAGAACTCCATCTGCGGCACTTTTTCGAGCGAGCGCAATTTGGCAGAGC 660  
Db 907 GTTCAGCCCGGAGAACTCCATCTGCGGCACTTTTTCGAGCGAGCGCAATTTGGCAGAGC 966  
Qy 661 GAAATAGTCGAAAGATTTACGGAATACGCTTATGTTTACAGTTCTGTCGCGGATG 720  
Db 967 GAAATAGTCGAAAGATTTACGGAATACGCTTATGTTTACAGTTCTGTCGCGGATG 1026  
Qy 721 GCAGTGATCAGTATGCTTCTCAAAATCTTGCAGAAAGTGTCAAAAGACATGATCATC 780  
Db 1027 GCAGTGATCAGTATGCTTCTCAAAATCTTGCAGAAAGTGTCAAAAGACATGATCATC 1086



QY 781 CAAAATGCTCAATTCGTCAATCACTGACACAAAAGCAGAGAAGTGTGCGAGCTACCGA 840  
DB 1087 CAAAATGCTCAATTCGTCAATCACTGACACAAAAGCAGAGAAGTGTGCGAGCTACCGA 1146  
QY 841 AAGAAGAAAGTGAATATATATTTCTAAATGCAATGGTGTGTGCAATTTATCGGGTGTGTGTTG 900  
DB 1147 AAGAAGAAAGTGAATATATATTTCTAAATGCAATGGTGTGTGCAATTTATCGGGTGTGTGTTG 1206  
QY 901 CCTTTAACAATTAATCAATTTGGTCAAGATTTTAAAAAGAGCCGAATGGCTAAACCGT 960  
DB 1207 CCTTTAACAATTAATCAATTTGGTCAAGATTTTAAAAAGAGCCGAATGGCTAAACCGT 1266  
QY 961 CAGCGGTCTCTGCGCAATAAATGCTCAAGTATAGCCATGTCCTTAGTCTGCGAAC 1020  
DB 1267 CAGCGGTCTCTGCGCAATAAATGCTCAAGTATAGCCATGTCCTTAGTCTGCGAAC 1326  
QY 1021 CCTCTGCTATTTCTTTGGCTGACACGAAAAAAGAGTTCGGAATGTCGAAAAATATCTC 1080  
DB 1327 CCTCTGCTATTTCTTTGGCTGACACGAAAAAAGAGTTCGGAATGTCGAAAAATATCTC 1386  
QY 1081 AACTCAACAGAGGTTGCAAAAAAGCAGAGTGTGGAATGCGAGGATCCAGCTACAC 1140  
DB 1387 AACTCAACAGAGGTTGCAAAAAAGCAGAGTGTGGAATGCGAGGATCCAGCTACAC 1446  
QY 1141 GACCTCTCCGACCTCTACTCAATTCGACAGATGTCGAGGCAACTCTTTCTA 1193  
DB 1447 GACCTCTCCGACCTCTACTCAATTCGACAGATGTCGAGGCAACTCTTTCTA 1499

## RESULT 3

US-09-721-870-106  
; Sequence 106, Application US/09721870  
; Patent No. 6632621  
; GENERAL INFORMATION:  
; APPLICANT: Lowery, David E.  
; APPLICANT: Geary, Timothy G.  
; APPLICANT: Kubiak, Teresa M.  
; APPLICANT: Larsen, Martha J.  
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 28341/6223  
; CURRENT APPLICATION NUMBER: US/09/721,870  
; CURRENT FILING DATE: 2000-11-24  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 106  
; LENGTH: 1301  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1299)  
; FEATURE:  
; OTHER INFORMATION: Clone identifier: CEGPCR19.1  
US-09-721-870-106

Query Match 93.0%; Score 1109; DB 3; Length 1301;  
Best Local Similarity 94.2%; Pred. No. 0;  
Matches 1193; Conservative 0; Mismatches 0; Indels 74; Gaps 1;  
QY 1 ATGGTTAGTTCGGCGCCACCAATTCGACCAATTCACCAACGACTCCCTCCACCATC 60  
DB 1 ATGGTTAGTTCGGCGCCACCAATTCGACCAATTCACCAACGACTCCCTCCACCATC 60  
QY 61 AGCAAGTTATCACAAGTCAATTCGAACAATGGCTCGTCAATTCAGATCGCTGAGGCGAAT 120  
DB 61 AGCAAGTTATCACAAGTCAATTCGAACAATGGCTCGTCAATTCAGATCGCTGAGGCGAAT 120  
QY 121 GCGGCAACAGGATCATGATATTAATCTAGATCTTTTACATCCGATCAATCTTCAATTC 180  
DB 121 GCGGCAACAGGATCATGATATTAATCTAGATCTTTTACATCCGATCAATCTTCAATTC 180  
QY 181 CTCTACGGGTCTCTGTTGATATAGGCATTTTGGAAACGGCGGCTACTATGCGGGTGTG 240

DB 181 CTCTACGGGTCTCTGTTGATATAGGCATTTTGGAAACGGCGGCGTACTATGCGGGGTG 240  
QY 241 GCGAGAAAAAAGAGCGGCTCCAAATCGGCTCGCAACGTAATTTCTGCTCAACTTGATCTTCACC 300  
DB 241 GCGAGAAAAAAGAGCGGCTCCAAATCGGCTCGCAACGTAATTTCTGCTCAACTTGATCTTCACC 300  
QY 301 GATTTGATATTTGGTGTTCACAGGATTCAGTCACACCAATGGTACCGGATGACCAAGAC 360  
DB 301 GATTTGATATTTGGTGTTCACAGGATTCAGTCACACCAATGGTACCGGATGACCAAGAC 360  
QY 361 TGGGCATTCGGGTCAAGTGTGCGCAATTTAGTCTCTTTGTCAAATTCGTTGTCGGTGTGTT 420  
DB 361 TGGGCATTCGGGTCAAGTGTGCGCAATTTAGTCTCTTTGTCAAATTCGTTGTCGGTGTGTT 420  
QY 421 GTGCGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGATATCAACGATCCC 480  
DB 421 GTGCGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGATATCAACGATCCC 480  
QY 481 ACCAAACAACCAAGTTTCTATTCTGTCAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540  
DB 481 ACCAAACAACCAAGTTTCTATTCTGTCAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540  
QY 541 TCAACACTGATATACTACCGTATCTTATGCTCTTTGCGAGCAGTCGATGGAAGCTTTTAC 600  
DB 541 TCAACACTGATATACTACCGTATCTTATGCTCTTTGCGAGCAGTCGATGGAAGCTTTTAC 600  
QY 601 GTTCAGCCCGAGAAAACTCCATACTGCGGGCACTTTTGGCAGCAGCGAATGGCAGAGC 660  
DB 601 GTTCAGCCCGAGAAAACTCCATACTGCGGGCACTTTTGGCAGCAGCGAATGGCAGAGC 660  
QY 661 GAAATAGTCGAAAGATTTACCGAATACGGTTATGTTTACATGTTTCTGTCGTCGCGCATG 720  
DB 661 GAAATAGTCGAAAGATTTACCGAATACGGTTATGTTTACATGTTTCTGTCGTCGCGCATG 720  
QY 721 CAGATGATCAGCTATTGCTACTTTCAAAATCTTGCAGAAAGTGTCAAAAGACATGATCANT 780  
DB 721 CAGATGATCAGCTATTGCTACTTTCAAAATCTTGCAGAAAGTGTCAAAAGACATGATCANT 780  
QY 781 CAAAATGCTCAATTTCTGTCAAATCACTGACACAAAAGCAGAGAAGTGTGCGAGCTCACGA 840  
DB 781 CAAAATGCTCAATTTCTGTCAAATCACTGACACAAAAGCAGAGAAGTGTGCGAGCTCACGA 840  
QY 841 AAGAAGAAAGTGAATATATTTCTAAATGCAATGGTGTGTGCAATTTATCGGGTGTGTGTTG 900  
DB 841 AAGAAGAAAGTGAATATATTTCTAAATGCAATGGTGTGTGCAATTTATCGGGTGTGTGTTG 900  
QY 901 CCTTTAACAATTAATCAATTTGGTCAAGATTTTAAAAAGAGCCGAATGGCTAAACCGT 960  
DB 901 CCTTTAACAATTAATCAATTTGGTCAAGATTTTAAAAAGAGCCGAATGGCTAAACCGT 960  
QY 961 CAGCGGTCTCTGCGCAATAAATGCTCAAGTATAGCCATGTCCTTAGTCTGCGAAC 1020  
DB 961 CAGCGGTCTCTGCGCAATAAATGCTCAAGTATAGCCATGTCCTTAGTCTGCGAAC 1020  
QY 1021 CTCTGCTATTTCTTTGGCTGACGAAAAAAGAGTTCGGAATGTCGAAAAATATCTC 1080  
DB 1021 CTCTGCTATTTCTTTGGCTGACGAAAAAAGAGTTCGGAATGTCGAAAAATATCTC 1080  
QY 1081 AACTCAACAG 1193  
DB 1081 AACTCAACAGATTTGTCCTGTTGCGAGTACAGTGAAGTGAATCTCGAATCGGCGGTCA 1140  
QY 1091 -----AGGGTTTCAAAAAAGCAGGTTCTGGAATTCGCGAG 1126  
DB 1141 AGGTTTTCGAGAAAAAATATTGACAGGGTTTCGAAAAAGCAGGTTCTGGAATTCGCGAG 1200  
QY 1127 GATCCAGGTACAGACCTCTCCGACCTCTACTCATTTGCGACAGATGTGCGAGCAACT 1186  
DB 1201 GATCCAGGTACAGACCTCTCCGACCTCTACTCATTTGCGACAGATGTGCGAGCAACT 1260  
QY 1187 CTTTCTA 1193  
DB 1261 CTTTCTA 1267

## RESULT 4

```
US-09-721-870-21
; Sequence 21, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/09/721,870
; CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 21
; LENGTH: 1130
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1128)
; FEATURE:
; OTHER INFORMATION: Clone identifier: CEGPCR4
US-09-721-870-21

Query Match      8.1%; Score 96.6; DB 3; Length 1130;
Best Local Similarity 47.0%; Pred. No. 1.3e-20;
Matches 438; Conservative 0; Mismatches 454; Indels 39; Gaps 3;

QY 136 GATGATATACGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGTTCCTG 195
DB 52 GAAGATTTGTCTCAAGGTGGTACATAATGTTAGTGTTCCTACCTGATATC 111
QY 196 TTGTGATTAGGCATTTTGGAAACGGCGCTACTATGGCGGTGGCGAGAAACAAGCG 255
DB 112 ATTGGCGCGGAATTAATGGAAATCACTCATGTGTGATTTTGGCAATCACAAGGAACAATCA 171
QY 256 CTCGAATCGGCTCGCAAGATATTTCTGCTCAACTTGAATCTTCACCGATTTGATATGGTG 315
DB 172 CTTCAAACTGTTCCGAATCTGTTTATCTTCTTTATCATGTTCTGATATTTGGTATGC 231
QY 316 TTCACGCGATTCAGTCACACATGGTACGGATGACCAAGACCTGGCATTCGGGTCA 375
DB 232 TGCACATCTGCAACAATCACTCCGATTAATGCAATCAAGAAAGATGGATCTTTGGAGAG 291
QY 376 GTGATGTGCAATTTAGTTCCTTTGTCAAAATTCGTTTCGGTGTGTTGTGACGAGTTGGAGC 435
DB 292 GCTTTATGCGGAATTCACCATTCATTTGCTGTATCAGCCTTTGTTCTCACTTTCACA 351
QY 436 CTCACGTGAATCTCCTTAGATAAATTTTGGCAATATCAACGATCCCAACCAACAACAGTT 495
DB 352 TTGACTGCAATCTCCATCAGACATACATCCTGATTCGATTTCCGATGAGGAAACCTATT 411
QY 496 TCTATTCGTCAAGCGTTGGCAATACATTTCTTATCTGATAGTCTCAACATGATATAT 555
DB 412 ACGCATATCAAGCGGTGGAGTGAATGCTATTTATTTTGGCGCTTTTGTCTCAACCATCA 469
QY 556 CTCACGTATCTTATGCTTTTCAGACACGTCCGATGGAAGCTTTTACGTTCAAGCCCGAGAA 615
DB 470 -----CATCCCAATTAATGTTCAAGCAAAAGCTGGGAGAGTTTGAGAT----- 513
QY 616 ACTCCATATCGCGGCACTTTTTCGACGAGGCGAATTTGGCAGACGCAAAATAGTCCGAAG 675
DB 514 -----TTTGTGGGCGAGTACTGACGCGAAACTGGGGAGCCAAATGAAGCCGAGAAAA 567
QY 676 ATTTACGGAATCAAGGTATGTTTACAGTTGCTGTCGCGATGTCAGTGTGATCAGTAT 735
DB 568 ATTTATGGTGACGCTGATGTTTCTTCAGCTCGTCAATCCCGCTTACCATCATCATATA 627
QY 736 TGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATCCAAAATGCTCAATTC 795
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DB 628 TCCTACACTCGGATTTCTTTTGAAGATCGGACAAAGCATGATTTCTCAAAGGGCGGAAAAG 687
QY 796 TGTCAATCACTGA-----CACAAAGACGAGAGAGTATGCGACGTCACGA 840
DB 688 CAAAAAAGACAGCAATTTGGGAAATGGAATTAAGTGATCAACAAAGAAATCGCTGTGAAGAGA 747
QY 841 AAGAAGAAAGTGAATATATTTCTAAATTCGAATGGTTGTTCACATTTATCGGGTGTGGTTG 900
DB 748 AGACAAGAAGTAAATAGAAATGCTTTATTTGGTATGTTAGTTCGCAATTCGGTTCAGCTGGATT 807
QY 901 CTTTAAACATTAATCAATTTGGTCAAGATTTTAAAAAAGAGCCCGAATGCGTAAACGT 960
DB 808 TGGTCAGTGACGTTCAACATTTCTGAGGACATATGAATATTTTGGCCAGAGCTCATCAAAACT 867
QY 961 CAGCGGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGCTCTTAGTGTCTGGGAC 1020
DB 868 CAAGAATATATCTTTTGGAAATTTGCTACACATTTGCAATTTGCAATGACCTCAACGGTATGGAAC 927
QY 1021 CCTCTGCTATTCTTTTGGCTGACACGAAAC 1051
DB 928 CGTTACTCTACGAGTGCTCAACCTCCAC 958

RESULT 5
US-09-721-870-35
; Sequence 35, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/09/721,870
; CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 35
; LENGTH: 1098
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1095)
; FEATURE:
; OTHER INFORMATION: Clone identifier: CEGPCR16
US-09-721-870-35

Query Match      7.0%; Score 84; DB 3; Length 1098;
Best Local Similarity 50.5%; Pred. No. 1.6e-16;
Matches 204; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

QY 167 CAATCTTCACATTCCTCTACGGGTTCTGTTTGTATTAAGGCATTTTGGAAACGGCGG 226
DB 86 CGATCTTTGCAACCATCTACATAATAATTTGTTAGTTGGCGTAACCGCAATTTGTTAG 145
QY 227 TACTATGGCGGTGGCGAGAAACAAGCGGCTCCAAATCGGCTCGCAACGATATTTCTGCTCA 286
DB 146 TAGTGATGTCGTGATGAGGTTTCAAGTTCTTCAATCATGTCAGGAACATGTTTCATCGTAT 205
QY 287 ACTTGATCTTCAACCATTTGATATTTGGTGTTCACAGCGATTCACACCATGTTAGTACG 346
DB 206 CTTTGTCAAGTTCTACATTTTGTGGCGATTTGTTAGTGTTCAGTAACCGCAATACCG 265
QY 347 CGATGACCAAGACGTGGCGATTCGGGTTCAGTGATGTCATTTAGTTCCTTTGTCAAAAT 406
DB 266 CATTCTCTAAAGTTGGTTATTTGGTGGACCAATGTTGTCATTTACTACCTTTGTTACAG 325
QY 407 CGGTGTCGGTGTGTCGAGGCTCCTCAGTTCGCAATCTCCTTAGATAAATTTCTGC 466
DB 326 GTACCGCGTTGAGTTTTCACGTTAAACGCTCACCGCAATTTGCAATTTGACATATATTC 385
```

QY 467 ATATCAACGATCCACCAACACCACTTCTATTCTGTAAGCTTGGCAATACATTTTC 526  
Db 386 TCATCTGTCATCCGACGAAAGAACCGATACGCAAGATCAAGCAATCGAAATGATAGTT 445  
QY 527 TTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATG 570  
Db 446 TCAACAGCGCCACTCAGTTGGGCTTTCGGTACCAATTAATTCATG 489

## RESULT 6

US-09-721-870-15  
; Sequence 15, Application US/09721870  
; Patent No. 6632621  
; GENERAL INFORMATION:  
; APPLICANT: Lowery, David E.  
; APPLICANT: Geary, Timothy G.  
; APPLICANT: Kubiak, Teresa M.  
; APPLICANT: Larsen, Martha J.  
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 28341/6223  
; CURRENT APPLICATION NUMBER: US/09/721,870  
; CURRENT FILING DATE: 2000-11-24  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 1352  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1350)  
; FEATURE:  
; OTHER INFORMATION: Clone identifier: CEGPCR14  
US-09-721-870-15

Query Match 6.6%; Score 78.8; DB 3; Length 1352;  
Best Local Similarity 47.4%; Pred. No. 9.2e-15;  
Matches 381; Conservative 0; Mismatches 402; Indels 21; Gaps 4;

QY 134 TCAGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCAATTCCTCTACGGGTTC 193  
Db 56 TCATGATTGGACAGTCCCTTTTGAAGTTGGCTTGGATATTCAGTACTATATCTTCTCA 115  
QY 194 TGTTCGTATTAGGCAATTTTGGAAACGGCGGCGTACTATGGGGGTGGGAGAAACAAGC 253  
Db 116 TATTATAATACGATTTGGTGGAAATGGGCTATTGATCACTTCAATTTTAAATCGGAAAGA 175  
QY 254 GGCTCCAATCGGCTCGCAAGTATTCTGCTCAACTTGATCTTACCGGATTTGATATTGG 313  
Db 176 AACTTTCGGTGGC---AAACATATCTTGATAAACCTGGGAGTTTCTGATTTGCTTCTTT 232  
QY 314 TGTTCACAGCGAATTCAGTGCACACCATGGTACCGGATGACCAAGACTGGGCATTCGGGT 373  
Db 233 GCATCAGCGGGTGGCGATCACTCCAGTATTCGCGTTTATGAGCGATGGATTTGGAA 292  
QY 374 CAGTGATGCGCAATTTAGTTCCTTTGTCGTAATTCGATTCGCGTGGTGTGACGAGTTGGA 433  
Db 293 TAAATATGTGTAATTTGGTTTCCAACTTGT CAGCGGTTTTCGGTGTCTCAATTTCTTCATGGT 352  
QY 434 GCTCACTCAATCTCTTAGATAAATTTCTGATATCAACGATCCCAACCAACACCCAG 493  
Db 353 CTTTGTGTTACATCGCAATTTAGATATCGAAGTATTTGTGACGCCACTCCGGGAACCCAT 412  
QY 494 TTTCTATTCTGTCAGCGTTGGCAATAACATTTCTTATCTGGATAGTCTCAACACTGATAA 553  
Db 413 GGTCTGATAGGATGCAAGTGGCTTCTGATGTTTACATGGGGTGGTTCGCTTCTTGTGCTA 472  
QY 554 ATCTACCGTATCTTATGTCCTTTTCGAGCAGTGTGATGGAAGCTTTTATAGTTTCAGCCGGAG 613  
Db 473 GT-----TATCCTCTATATTACTACAGAACTTGAAGAAACAATGGTTATTGA-----AA 520  
QY 614 AAATCCATCTACTCGGGGCACTTTTGGCAGCGGCAATTTGGCAGAGCGGAATAGTCGAA 673

Db 521 ATGTGACATTTATGTGGAGATTTTTTGGCGGAGTTCAATTTGGCAGTCCGATGAATATCCA 580  
QY 674 AGATTTTACGGAACCTACGGTTATGTTGTATACAGTTTCGTGCGCGATGGCAGTGCATCACGT 733  
Db 581 AGTTGACATATACTACGAGTTTATGATTTATTCAGCTGATTTATCCAGCAATATCATGT 640  
QY 734 ATTGCTACTTCAAAATCTTGGCAAAAGTGTCAAAAGACATGATCATCCAAAATGCTCAAT 793  
Db 641 CTTTTTGTATTAAATGATTTCTACAAAAGGTACAAAACCGACTGGCTTGTGACAGGGAT 700  
QY 794 TCTGTCAATCACTGACACAAAAGCAGAGAGTATGGGAGCTCACGAAAGAAAGTGA 853  
Db 701 CCATGTTGACTGCGCGCACACAGGCTCAAAACAGCAG-----TTCGAAAGCGACGAGTGA 754  
QY 854 ATTATATTCTTAATTGCAATGGTTGTCACATTTATCGGTTGTTGTTGCGCTTTTAAACATTAC 913  
Db 755 TGTACGTTGTTGATTTCTAATGGTTATTTGTTTATGCTTGTGTTCCCGTTTCCGCG 814  
QY 914 TCAATTTGGTCAAGATTTTAAAA 937  
Db 815 TGAATTTGTTTCAGAGATCTCGGAA 838

## RESULT 7

US-09-721-870-25  
; Sequence 25, Application US/09721870  
; Patent No. 6632621  
; GENERAL INFORMATION:  
; APPLICANT: Lowery, David E.  
; APPLICANT: Geary, Timothy G.  
; APPLICANT: Kubiak, Teresa M.  
; APPLICANT: Larsen, Martha J.  
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 28341/6223  
; CURRENT APPLICATION NUMBER: US/09/721,870  
; CURRENT FILING DATE: 2000-11-24  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 1374  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1371)  
; FEATURE:  
; OTHER INFORMATION: Clone identifier: CEGPCR7  
US-09-721-870-25

Query Match 5.6%; Score 66.6; DB 3; Length 1374;  
Best Local Similarity 48.3%; Pred. No. 8.9e-11;  
Matches 186; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 180 CCTCTACGGTTCCTGTTGTTGTTATAGGCATTTTGGAAACGGCGGCTACTATGGCGGT 239  
Db 93 CGTGACCTTTTCTCTTTTCTTTTCTTTGGACTCTTTGGAAATGTGACCTTGATTTACGTAAC 152  
QY 240 GCGGAGAAACAAGCGCTCCATCGCTCGCAACGATTTTCTGCTCAACTGATCTTCTAC 299  
Db 153 TTGAGCCATAAAGCTTTTACTGAGCGTTTCAAAACATATTCATCTGAACTCGCGGCGAG 212  
QY 300 CGATTTGATTTGTTGTTTTCACAGCGATTCAGTGCACCATGTTAGCGGATGACCAAGAA 359  
Db 213 CGATTTGATGATGTGCATATTATCGCTTCCATCACTCCAAATCACAAATGTTGACAAA 272  
QY 360 CTGGCGATTCGGGTGAGTGTGCGATTTAGTTCCTTTGTTCAAAATTCGTTGTTGTTGTT 419  
Db 273 CTGTACTTTTGGAAATCTACTCTGCCATTTGATACCATGCAATTCAGGATATCAGCATTTT 332  
QY 420 TGTGAGGATTTGGCGCTCACCTGCAATCTCTTAGTAAATTTCTGCAATATCAACGATCC 479  
Db 333 CGTATGCAATTCAGTCTCGGTGCGAATGCTTTGGATCGGTATATCTTTGTAGTAGACC 392

QY 480 CACCAACACACAGTTTCTATTGTCGTCAGCGTTGGCAATAACATTTCTTATCTGCATAGT 539  
Db |||||  
QY 393 ACAATCTTACACACTATCCAAAGAGGAGCATTTCTTACTACTGTCTATTGTGGATCCT 452  
Db |||||  
QY 540 CTCACACTGATAAATCTACCGTAT 564  
Db |||||  
QY 453 CTCCTTTGTGTAATCTACCCCTAT 477  
Db |||||

## RESULT 8

US-09-255-368-5  
; Sequence 5, Application US/09255368  
; Patent No. 6262246  
; GENERAL INFORMATION:  
; APPLICANT: Gerald, Christophe P.G.  
; APPLICANT: Jones, Kenneth A.  
; APPLICANT: Bonini, James A.  
; APPLICANT: Borowsky, Beth  
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors  
; FILE REFERENCE: 1795/57155-A  
; CURRENT APPLICATION NUMBER: US/09/255,368  
; EARLIER FILING DATE: 1999-02-22  
; EARLIER FILING DATE: 1998-09-25  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0 - beta  
; SEQ ID NO 5  
; LENGTH: 1302  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-255-368-5

Query Match 5.2%; Score 61.6; DB 3; Length 1302;  
Best Local Similarity 46.3%; Pred. No. 3.7e-09;  
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

QY 165 ATCAATCTTCACATTCCTCTACGGGTTCTGTTGTTATTTAGGCATTTTGGAAACGGCGG 224  
Db |||||  
QY 165 AGCAATCTTCATTTTCTCTACTTTCTGATCTCTTTTGTGCATGATGGGAATACTGT 224  
Db |||||  
QY 225 CGTACTATGGCGGTGGCGAGAAACAAAGCGGCTCCAAATCGGCTCGCAAGCTATTTCTGCT 284  
Db |||||  
QY 225 GGTTCGCTTATGTAATGAGGNAACAACATATGCACACAGTCACATCTCTTCATCTT 284  
Db |||||  
QY 285 CAACCTGATCTTCAACGATTTGATATGTTGTTCAAGCGATTCACAGTCCACCATGGTA 344  
Db |||||  
QY 285 AAACCTGGCCATAAGTGAATTTACTAGTTGGCATATTTCTGCATGCCCTATAACACTGCTGA 344  
Db |||||  
QY 345 CGCGATGACCAAGACTGGGCTCGGTCAGTGATGGCCATTTAGTTCTTGTGTCAAA 404  
Db |||||  
QY 345 CAATATTTATAGCAGGATGGCCATTTGGAAACAGATGTGCAAGATCAGTGGATTTGTCCA 404  
Db |||||  
QY 405 TTCTGTTGCGGTGTTGTCAGAGTGGAGCGCTCACTGCAATCTCTCTAGATAAAATTTCT 464  
Db |||||  
QY 405 GGGATATCTGTGCGAGCTTCAGTCTTTACGTTAGTTGCAATTTGCTAGATAGGTTCGA 464  
Db |||||  
QY 465 GCATATCAACGATCCCAACCAACAGCTTCTTATTCGTCAGGTTTGGCAATAAATTTCT 524  
Db |||||  
QY 465 GTGTGTTGCTTACCCCTTTTAAACCAAGCTCACTATCAAGACAGCGTTTGTCTATTTAT 524  
Db |||||  
QY 525 TCTTATCTGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTTCGACACGT 584  
Db |||||  
QY 525 GATCATCTGGGTCCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCA 584  
Db |||||  
QY 585 CGATGGAAGCTTTTAC 600  
Db |||||  
QY 585 AGAAGAAAATATTAC 600  
Db |||||

## RESULT 9

US-09-405-558-5  
; Sequence 5, Application US/09538036  
; Patent No. 6849727  
; GENERAL INFORMATION:  
; APPLICANT: Gerald, Christophe P.G.  
; APPLICANT: Jones, Kenneth A.  
; APPLICANT: Bonini, James A.  
; APPLICANT: Borowsky, Beth E.  
; APPLICANT: Craig, Douglas A.  
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors

; Sequence 5, Application US/09405558A  
; Patent No. 6709831  
; GENERAL INFORMATION:  
; APPLICANT: Gerald, Christophe P.G.  
; APPLICANT: Jones, Kenneth A.  
; APPLICANT: Bonini, James A.  
; APPLICANT: Borowsky, Beth E.  
; APPLICANT: Craig, Douglas A.  
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors  
; FILE REFERENCE: 57155-C  
; CURRENT APPLICATION NUMBER: US/09/405,558A  
; EARLIER FILING DATE: 1999-09-24  
; EARLIER FILING DATE: 1998-09-25  
; EARLIER FILING DATE: 1998-09-25  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn Ver. 2.0 - beta  
; SEQ ID NO 5  
; LENGTH: 1302  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-405-558-5

Query Match 5.2%; Score 61.6; DB 3; Length 1302;  
Best Local Similarity 46.3%; Pred. No. 3.7e-09;  
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

QY 165 ATCAATCTTCACATTCCTCTACGGGTTCTGTTGTTATTTAGGCATTTTGGAAACGGCGG 224  
Db |||||  
QY 165 AGCAATCTTCATTTTCTCTACTTTCTGATCTCTTTTGTGCATGATGGGAATACTGT 224  
Db |||||  
QY 225 CGTACTATGGCGGTGGCGAGAAACAAAGCGGCTCCAAATCGGCTCGCAAGCTATTTCTGCT 284  
Db |||||  
QY 225 GGTTCGCTTATGTAATGAGGNAACAACATATGCACACAGTCACATCTCTTCATCTT 284  
Db |||||  
QY 285 CAACCTGATCTTCAACGATTTGATATGTTGTTCAAGCGATTCACAGTCCACCATGGTA 344  
Db |||||  
QY 285 AAACCTGGCCATAAGTGAATTTACTAGTTGGCATATTTCTGCATGCCCTATAACACTGCTGA 344  
Db |||||  
QY 345 CGCGATGACCAAGACTGGGCTCGGTCAGTGATGGCCATTTAGTTCTTGTGTCAAA 404  
Db |||||  
QY 345 CAATATTTATAGCAGGATGGCCATTTGGAAACAGATGTGCAAGATCAGTGGATTTGTCCA 404  
Db |||||  
QY 405 TTCTGTTGCGGTGTTGTCAGAGTGGAGCGCTCACTGCAATCTCTCTAGATAAAATTTCT 464  
Db |||||  
QY 405 GGGATATCTGTGCGAGCTTCAGTCTTTACGTTAGTTGCAATTTGCTAGATAGGTTCGA 464  
Db |||||  
QY 465 GCATATCAACGATCCCAACCAACAGCTTCTTATTCGTCAGGTTTGGCAATAAATTTCT 524  
Db |||||  
QY 465 GTGTGTTGCTTACCCCTTTTAAACCAAGCTCACTATCAAGACAGCGTTTGTCTATTTAT 524  
Db |||||  
QY 525 TCTTATCTGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTTCGACACGT 584  
Db |||||  
QY 525 GATCATCTGGGTCCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCA 584  
Db |||||  
QY 585 CGATGGAAGCTTTTAC 600  
Db |||||  
QY 585 AGAAGAAAATATTAC 600  
Db |||||

## RESULT 10

US-09-538-036-5  
; Sequence 5, Application US/09538036  
; Patent No. 6849727  
; GENERAL INFORMATION:  
; APPLICANT: Gerald, Christophe P.G.  
; APPLICANT: Jones, Kenneth A.  
; APPLICANT: Bonini, James A.  
; APPLICANT: Borowsky, Beth E.  
; APPLICANT: Craig, Douglas A.  
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors

```
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: 57155-D/JPW
; CURRENT APPLICATION NUMBER: US/09/538,036
; CURRENT FILING DATE: 2000-03-29
; EARLIER APPLICATION NUMBER: 09/405,558
; EARLIER FILING DATE: 1999-09-24
; EARLIER APPLICATION NUMBER: 09/255,368
; EARLIER FILING DATE: 1999-02-22
; EARLIER APPLICATION NUMBER: 09/161,113
; EARLIER FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1302
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-538-036-5

Query Match          5.2%; Score 61.6; DB 3; Length 1302;
Best Local Similarity 46.3%; Pred. No. 3.7e-09;
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

QY 165 ATCAATCTTCACATTCCTCTACGGGTTCTCTGTTTGTATTAGGCATTTTGGAAACGGCGG 224
    |||||
Db 165 AGCAATCTTCATTTATTCCTACTTCTGATCTTCTTTGTGCAATGAGTGGAAATACTGT 224

QY 225 CGTACTATGGCGGCGGAGAAACAAGCGGCTCCAAATCGGCTCGCAACGTATTTCTGCT 284
    |||||
Db 225 GGTTCGCTTTATTTGTAATGAGGAACAACAATATGCACAGTCACTAATCTCTTCATCTT 284

QY 285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTGCACACCATGGTA 344
    |||||
Db 285 AAACCTGGCCATAAGTGAATTTACTAGTTGGCATATTCTGCATGCCCTATACACTGCTGGA 344

QY 345 CGCGATGACCAAGACTGGGCATTCGGGTCAGTGATGTGCAATTTAGTTCTTTGTCAA 404
    |||||
Db 345 CAATATTATAGCAGGATGCCATTTGGAAACAGATGTGCAAGATCAGTGGATGGTCCA 404

QY 405 TTGCTGTTGCTGTTTGTGACAGAGTTGGAGCCCTCACTGCAATCTCCTTAGATAAAATTTCT 464
    |||||
Db 405 GGGAAATATCTGTCGAGCTTCAGTCTTTACGTTAGTTGCAATTTGCTGTAGATAGGTTCCA 464

QY 465 GCATATCAACGATGCCACCAACAACAGTTTCTATTCTCGTCAAGCGTTGCCATACATT 524
    |||||
Db 465 GTGTGTGGTCTACCCCTTTTAAACCAAGCTTCATATCAAGACAGCGTTGTCAATTATTAT 524

QY 525 TCTTATCTGGATAGTCTCAACACTGTATAAATCTACCGTATCTTATGTTCTTTGAGCACGT 584
    |||||
Db 525 GATCATCTGGTCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCA 584

QY 585 CGATGGAAGCTTTTAC 600
    |||||
Db 585 AGAAGAAAAAATATTAC 600

RESULT 11
US-09-719-0888-4
; Sequence 4, Application US/09719088B
; Patent No. 6803232
; GENERAL INFORMATION:
; APPLICANT: Herzog, Herbert
; TITLE OF INVENTION: NPY-Y7 Receptor Gene
; FILE REFERENCE: 12020-0003
; CURRENT APPLICATION NUMBER: US/09/719,088B
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/AU99/00523
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: AU PP4385
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1903
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; TYPE: DNA
; ORGANISM: Homo sapiens NPY-Y7-encoding gene
; US-09-719-088B-4

Query Match          5.2%; Score 61.6; DB 3; Length 1903;
Best Local Similarity 46.3%; Pred. No. 4.7e-09;
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

QY 165 ATCAATCTTCACATTCCTCTACGGGTTCTCTGTTTGTATTAGGCATTTTGGAAACGGCGG 224
    |||||
Db 165 AGCAATCTTCATTTATTTCTACTTCTGATCTTCTTTTGTGCAATGAGTGGAAATACTGT 571

QY 225 CGTACTATGGCGGCGGAGAAACAAGCGGCTCCAAATCGGCTCGCAACGTATTTCTGCT 284
    |||||
Db 225 GGTTCGCTTTATTTGTAATGAGGAACAACAATATGCACAGTCACTAATCTCTTCATCTT 631

QY 285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTGCACACCATGGTA 344
    |||||
Db 285 AAACCTGGCCATAAGTGAATTTACTAGTTGGCATATTCTGCATGCCCTATACACTGCTGGA 631

QY 345 CGCGATGACCAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTTCTTTGTCAA 404
    |||||
Db 345 CAATATTATAGCAGGATGCCATTTGGAAACAGATGTGCAAGATCAGTGGATGGTCCA 751

QY 405 TTGCTGTTGCTGTTTGTGACAGAGTTGGAGCCCTCACTGCAATCTCCTTAGATAAAATTTCT 464
    |||||
Db 405 GGGAAATATCTGTCGAGCTTCAGTCTTTACGTTAGTTGCAATTTGCTGTAGATAGGTTCCA 811

QY 465 GCATATCAACGATGCCACCAACAACAGTTTCTATTCTCAAGCGTTGCCATACATT 524
    |||||
Db 465 GTGTGTGGTCTACCCCTTTTAAACCAAGCTTCATATCAAGACAGCGTTTGTCAATTATTAT 871

QY 525 TCTTATCTGGATAGTCTCAACACTGTATAAATCTACCGTATCTTATGTTCTTTGAGCACGT 584
    |||||
Db 525 GATCATCTGGTCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCA 931

QY 585 CGATGGAAGCTTTTAC 600
    |||||
Db 932 AGAAGAAAAAATATTAC 947

RESULT 12
US-09-693-746-1
; Sequence 1, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Metho
; TITLE OF INVENTION: Related To The Same
; FILE REFERENCE: 6297.lcp
; CURRENT APPLICATION NUMBER: US/09/693,746
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/425,676
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1803
; TYPE: DNA
; ORGANISM: D. melanogaster
; US-09-693-746-1

Query Match          5.0%; Score 60.2; DB 3; Length 1803;
Best Local Similarity 45.9%; Pred. No. 1.3e-08;
Matches 206; Conservative 0; Mismatches 243; Indels 0; Gaps 0;

QY 131 GCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTTCTCTACGGGT 190
    |||||
Db 155 GGAGCGGGGGATCATTCACACCAGTTGTCGCAAAATCTTCTTACGTCTCTGTAGCCCA 214
```

191 TCCTGTTGTTATTAGGCATTTTGGAAACGGCGGTACTATGCGCGGTGCGGAGAAC 250  
Db |||||  
215 CGGTCTTTGTCCTGGGTGTCCTCGGAATGTCCTGTTGCTACGTATGTTGAGATC 274  
Qy |||||  
251 AGCGCTCCAAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCAACCGATTGAT 310  
Db |||||  
275 GGGCCATCAGACTGTGACCAATATATTATCATCAGAACTCGCCCTGTGCGACATATTGC 334  
Qy |||||  
311 TGGTGTTCACAGCGATTCAGTCAACCATGTTAGCGGATGACCAAGACTGGGCAATTCG 370  
Db |||||  
335 TCTGGTCTCGCGGTGCAATTTACTCGGCTTTTACACGTTTACAGTTCATGCGTCTGCGGCTTCG 394  
Qy |||||  
371 GGTGATGATGCGCAATTTAGTTCCTTTGTCGAAATTCGTTGCGTGTGTTGTGACGATT 430  
Db |||||  
395 GAGGAGTCTGTGCCATCTGGTGTCTTTGCCCAGGATGCGATCTACATATCCAGC 454  
Qy |||||  
431 GGAGCTCACTGCAATCTCTTTAGATAAAATTTCTGCATATCAACGATCCCAACCAAC 490  
Db |||||  
455 TGACCTCACTCGATTCGCAATCGTACTTCGTTATCATATACCCCTTCATCCG 514  
Qy |||||  
491 CAGTTTCTATTGTCGAAGGTTGGCAATAAATTTCTTATCTGATAGTCTCAACACTGA 550  
Db |||||  
515 GCATGAAGCTCTCCACCTGCAATCGGATCATAGTGAAGCATCTGGGTGATAGCCCTGCTGG 574  
Qy |||||  
551 TAAATCTACCGTATCTTATGCTTTTCGAG 579  
Db |||||  
575 CCACCGTCTCCCTACGCGCATGATACATGAAG 603

## RESULT 13

US-09-676-970-1

; Sequence 1, Application US/09676970

; Patent No. 6372743

; GENERAL INFORMATION:

; APPLICANT: Darrow, James W.

; APPLICANT: De Lombaert, Stephane

; APPLICANT: Blum, Charles

; APPLICANT: Tran, Jennifer

; APPLICANT: Giangliordano, Mark

; APPLICANT: Griffith, David Andrew

; APPLICANT: Carpino, Philip Albert

; TITLE OF INVENTION: Certain Alkylene Diamine-Substituted Pyrazolo

; TITLE OF INVENTION: [1,5-a]-1,5-Pyrimidines and pyrazolo

; FILE REFERENCE: U012955-3

; CURRENT APPLICATION NUMBER: US/09/676,970

; PRIOR FILING DATE: 2000-09-29

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 1605

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-676-970-1

Query Match 4.8%; Score 57.8; DB 3; Length 1605;  
Best Local Similarity 46.4%; Pred. No. 7.3e-08;  
Matches 188; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

Qy 75 AAGTCATTGGAACATGGCTCGTGCAATTCAGATCGCTGAGGCGATGCGGCAACAGGCAT 134  
Db 226 AATCATTCAGTCCACTCTAAATTTCTCAGAGAAGATGCCAGCTTCTGGCTTTGAAA 285  
Qy 135 CGATGATATTACTGTAGACTTTTACATCCGATCGCTGATGATGATGATGATGATGAT 194  
Db 286 TGATGATTTGTCATCTGCGCTTGGCCATGATATTTACCTTAGCTCTTGTCTATGGAGTGT 345  
Qy 195 GTTGTATTAGGCATTTTGGAAACGGCGGTACTATGCGCGGTGGGAGAAACAAGCG 254  
Db 346 GATCATTTCTGGTGTCTCTGAAACCTGGCTTGTATCATATCATATCTTGAACAAGGA 405  
Qy 255 GCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGTATCTTCAACGATTTGATTTG 314  
Db 286 TGATGATTTGTCATCTGCGCTTGGCCATGATATTTACCTTAGCTCTTGTCTATGGAGTGT 345  
Qy 195 GTTGTATTAGGCATTTTGGAAACGGCGGTACTATGCGCGGTGGGAGAAACAAGCG 254  
Db 346 GATCATTTCTGGTGTCTCTGAAACCTGGCTTGTATCATATCATATCTTGAACAAGGA 405  
Qy 255 GCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGTATCTTCAACGATTTGATTTG 314

Db 406 GATGAGAAATGTTACCAACATCTGATTTGTGAACCTTTCTTCTCAGACTTGTCTTGTGC 465  
Qy 315 GTTTCACAGCGATTTCCAGTCCACCATGCGATGACCAAGACTGGGCAATTCGGGTC 374  
Db 466 CATCATGTGTCCTCCCTTTACATTTGTCTACATTAATGACCACTGGGTCTTTGTGGA 525  
Qy 375 AGTATGATGCGCAATTTAGTTCCTTTGTCAAATTCGTTTGGTGTGTTGTGACGAGTTGG 434  
Db 526 GGCGATGTTAAGTTGATCTTTTGTGCAATGTTTCAATCACTGTTGTCTCATTTTCTC 585  
Qy 435 CCTCAGTCAATCTCTTAGATAAAATTTCTGATATCAACGATCC 479  
Db 586 TCTGGTTCTCATTTGCTGTGGAACGACATCAGCTGATTAATCAACCC 630

## RESULT 14

US-09-676-972B-1

; Sequence 1, Application US/09676972B

; Patent No. 6476038

; GENERAL INFORMATION:

; APPLICANT: Darrow, James W.

; APPLICANT: De Lombaert, Stephane

; APPLICANT: Blum, Charles

; APPLICANT: Tran, Jennifer

; APPLICANT: Giangliordano, Mark

; APPLICANT: Griffith, David Andrew

; APPLICANT: Carpino, Philip Albert

; TITLE OF INVENTION: Amino Substituted Pyrazolo [1,5-a]-1,5-Pyrimidines and

; TITLE OF INVENTION: Pyrazolo [1,5-a]-1,3,5-Triazines

; FILE REFERENCE: U 012956-1

; CURRENT APPLICATION NUMBER: US/09/676,972B

; CURRENT FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: US 60/156,868

; PRIOR FILING DATE: 1999-09-30

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 1605

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-676-972B-1

Query Match 4.8%; Score 57.8; DB 3; Length 1605;  
Best Local Similarity 46.4%; Pred. No. 7.3e-08;  
Matches 188; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

Qy 75 AAGTCATTGGAACATGGCTCGTGCAATTCAGATCGCTGAGGCGATGCGGCAACAGGCAT 134  
Db 226 AATCATTCAGTCCACTCTAAATTTCTCAGAGAAGATGCCAGCTTCTGGCTTTGAAA 285  
Qy 135 CGATGATATTACTGTAGACTTTTACATCCGATCGCTGATGATGATGATGATGATGAT 194  
Db 286 TGATGATTTGTCATCTGCGCTTGGCCATGATATTTACCTTAGCTCTTGTCTATGGAGTGT 345  
Qy 195 GTTGTATTAGGCATTTTGGAAACGGCGGTACTATGCGCGGTGGGAGAAACAAGCG 254  
Db 346 GATCATTTCTGGTGTCTCTGAAACCTGGCTTGTATCATATCATATCTTGAACAAGGA 405  
Qy 255 GCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGTATCTTCAACGATTTGATTTG 314  
Db 406 GATGAGAAATGTTACCAACATCTGATTTGTGAACCTTTCTCTCAGACTTCTGTTTGC 465  
Qy 315 GTTTCACAGCGATTTCCAGTCCACCATGTTGATGCGGATGACCAAGACTGGGCAATTCGGGTC 374  
Db 466 CATCATGTGTCCTCCCTTTACATTTGTCTACACATTAATGGAACCACTGGGTCTTTGTGGA 525  
Qy 375 AGTATGATGCGCAATTTAGTTCCTTTGTCAAATTCGTTTGGTGTGTTGTGACGAGTTGG 434  
Db 526 GGCGATGTTAAGTTGATCTTTTGTGCAATGTTTCAATCACTGTTGTCTCATTTTCTC 585  
Qy 435 CCTCAGTCAATCTCTTAGATAAAATTTCTGATATCAACGATCC 479  
Db 586 TCTGGTTCTCATTTGCTGTGGAACGACATCAGCTGATTAATCAACCC 630



RESULT 15  
US-09-016-434-1231  
; Sequence 1231, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1231:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1605 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g189155  
US-09-016-434-1231

Query Match 4.8%; Score 57.8; DB 3; Length 1605;  
Best Local Similarity 46.4%; Pred. No. 7.3e-08;  
Matches 188; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

Qy	75	AAGTCATTGCAACATGGCTCGTCGATTCAGATCGCTGAGGCGATTGGGCGACAGGCAT	134
Db	226	AAATCATTCAGTCCACTCTAAATTTCTCAGAGAAGAATGCCAGCTTCCTGGCTTTGAAAA	285
Qy	135	CGATGATATTAAGTAGATTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCCT	194
Db	286	TGATGATGTCATCTGCCCTTGGCCATGATATTACCTTAGCTCTTGCTTATGGAGCTGT	345
Qy	195	GTTTGATATAGCATTTTGGAAACGGGGCGGTA CTATGGGCGGTGGGAGAAACAAGCG	254
Db	346	GATCATTTCTTGGTGTCTCTGGAAACCTGGCCCTTGATCATATCATCTTGAACAAAAAGA	405
Qy	255	GCTCCAATCGGCTCGCAAGATTTCTGCTCAACTGATCTTCACCGATTGATATTGGT	314
Db	406	GATGAAATGTTACCAACATCCTGAITGTGAAACCTTTCCTTCTCAGACTTGTCTTGTGC	465
Qy	315	GTTTCACAGCGAFTCCAGTCACACCATGGTACCGCATGACCAAGACTGGGCATTCGGGTC	374
Db	466	CATCATGTGCTCCCTTTTACATTTGTCTACACATTAATGGNCCACTGGGCTCTTGGTGA	525

Qy	375	AGTGATGTGCCAATTAGTTTCCTTTGTCAAATTCGGTTCGGTGTGTCGACGAGTTGGAG	434
Db	526	GGCGATGTGTAAGTTGAATCCTTTTGTGCAATGTGTTTCAATCACTGTGTCCATTTTCTC	585
Qy	435	CCTCACTGCAATCTCCTTAGATAAAATTTCTGCATATCAACGATCC	479
Db	586	TCTGGTTCTCATTTGCTGTGGAAACGACATCAGCTGATAATCAACCC	630

Search completed: May 8, 2006, 14:48:09  
Job time : 257 secs

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OM protein - protein search, using sw model

Run on: May 8, 2006, 09:29:53 ; Search time 41 Seconds  
(without alignments)  
931.660 Million cell updates/sec

Title: US-10-650-467-105  
Perfect score: 2074  
Sequence: 1 WVSSAATISTISTTTTPSTI.....QLHDLPTSTHSDRCAGNSP 397

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: Pir1.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	607.5	29.3	539	2 T27559	hypothetical prote
2	514	24.8	374	2 T19340	hypothetical prote
3	485.5	23.4	457	2 T29741	hypothetical prote
4	461.5	22.3	365	2 T20184	hypothetical prote
5	419.5	20.2	412	2 T22076	hypothetical prote
6	387.5	18.7	373	2 T24487	hypothetical prote
7	382	18.4	376	2 T19186	hypothetical prote
8	373.5	18.0	370	1 I52315	G protein-coupled
9	354	17.1	375	2 S63685	neuropeptide y rec
10	346.5	16.7	384	2 A45490	neuropeptide y pep
11	342	16.5	382	2 S27388	neuropeptide y rec
12	337	16.2	449	2 A41738	G protein-coupled
13	333	16.1	349	2 S12863	neuropeptide y pep
14	333	16.1	382	2 B46133	neuropeptide y pep
15	324	15.6	381	2 I39187	neuropeptide y pep
16	321	15.5	399	2 T16277	hypothetical prote
17	314	15.1	375	2 G02300	pancreatic polypep
18	314	15.1	375	2 I39182	neuropeptide y pep
19	310.5	15.0	366	2 S71152	neuropeptide y pep
20	305.5	14.7	504	2 A41783	tachykinin recepto
21	303.5	14.6	423	2 B40470	glucocorticoid-ind
22	295.5	14.2	391	2 T32714	hypothetical prote
23	292.5	14.1	391	2 C41795	somatostatin recep
24	292	14.1	428	2 S30508	probable G protein
25	290.5	14.0	443	2 A40470	glucocorticoid-ind
26	289	13.9	418	2 A46226	somatostatin recep
27	289	13.9	428	2 A44021	somatostatin recep
28	288.5	13.9	390	2 B41007	bombesin receptor,
29	286.5	13.8	391	2 A39297	somatostatin recep

30	284.5	13.7	391	2 A41795	somatostatin recep
31	284.5	13.7	423	2 JC7677	allatostatin recep
32	283.5	13.7	376	2 I50102	Phe13 bombesin rec
33	282.5	13.6	455	2 T15622	hypothetical prote
34	282	13.6	391	2 T32517	hypothetical prote
35	281.5	13.6	369	2 B41795	somatostatin recep
36	281	13.5	363	2 I57940	somatostatin recep
37	281	13.5	519	2 S17783	tachykinin recepto
38	280.5	13.5	349	2 I59336	galanin receptor 1
39	279.5	13.5	384	2 S20303	neurokinin 2 recep
40	279.5	13.5	385	2 S55524	neurokinin 3 recep
41	278	13.4	346	2 S29248	somatostatin recep
42	277.5	13.4	440	2 A44081	kappa-type opioid
43	276.5	13.3	384	2 A47249	brain-specific som
44	276.5	13.3	388	2 JN0605	somatostatin recep
45	276.5	13.3	394	2 JC7209	galanin receptor -

ALIGNMENTS

RESULT 1

T27559  
hypothetical protein ZC412.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T27559  
R:Ainscough, R.  
submitted to the EMBL Data Library, August 1996  
A:Reference number: Z20387  
A:Accession: T27559  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-539 <WIL>  
A:Cross-references: UNIPROT:Q23305; UNIPARC:UPI0000083344; EMBL:Z78067; PIDN:CA801528.1  
A:Experimental source: clone ZC412  
C:Genetics:  
A:Gene: CESP:ZC412.1  
A:Map position: 5  
A:Introns: 29/3; 75/3; 112/1; 144/3; 180/3; 223/3; 241/3; 324/3; 376/2; 426/2; 456/3

Query Match 29.3%; Score 607.5; DB 2; Length 539;  
Best Local Similarity 35.3%; Pred. No. 7.6e-44;  
Matches 119; Conservative 76; Mismatches 111; Indels 31; Gaps 7;

QY	33	CIQAEIAAQAQIDITVDVIRSIETFLYGLFVLGIFGNGGVLWAVARNKRLQSAENV	92
DB	9	CIDVNAIL--QQFNDWTVLFEVRLGYSVLYFLILLIIGLVGNLLITSLMRKKL-SVANI	65
QY	93	FLNLNIFTDLILVFTAIPTVPMYAMTKQWAFGSMVCHLVPLNSCSFVFTSMLFAISLD	152
DB	66	FLINLAVSDLLLCITAVETITPLAFMKRWIFGIIMCKLVPTCQAFSLVLISSNSLCVIAID	125
QY	153	KFLHNDTKQPVSRQALAITFLIWIYSTLINPLMSFEHVDGFSFYQPOET-----	206
DB	126	YSIVTPTLRFPWSDRHARWLLMFTWVAFLASYPL-----YYSQNLTKVNIENV	175
QY	207	PYCGHFCDEANWQSNRSKI-YGTTVMLLQFVPMVAVITYCYFKILQKVSKDMIQNAQF	265
DB	176	TLCGDFCGEFNQSDSEISKLYTTSLLIIQLIIPAINSPCYLMILQKVQTDWLVDGSM	235
QY	266	QCSLTQKQRSDATSRKKVNYILIAMVVTFIGMPLPLTLNLVKDKFKKEPEV-----	317
DB	236	--LTAQAQAQTAVAKRRVMTVILMWIVFMACWFFLSAVNLFRLDGRMFECQFVYKVL	292
QY	318	LKRQPPFWAINAHVITAMSLVWNPLLPWLTRKQKRS	354
DB	293	MWDQMYPKLLNVHVITAMTSIVWNPVLYFWMKRRHRA	329

RESULT 2

T19340  
hypothetical protein C16D6.2 - Caenorhabditis elegans



Db 227 GSO--KELSEARRQTORLRTNRMLIIMTVFALSWSLPSVGFNRLDYSAALPGIDISQ 284  
QY 322 PFFMAINAHVIAVMSLVVMPFLFFWLTTRKQKRSGLSKILNSTRGSKAGSGSLRGI 377  
Db 285 DYLFGLIIFHCISMTSVVNPFLGY-CNEHFRAFAALDITVKA-----CGNERV 334  
RESULT 5  
T22076  
hypothetical protein F41E7.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T22076  
R:Lenard, N.  
submitted to the EMBL Data Library, November 1995  
A:Reference number: Z19509  
A:Accession: T22076  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-412 <WIL>  
A:Cross-references: UNIPROT:Q20275; UNIPARC:UPI000017663A; EMBL:Z68106; PIDN:CAA92126.1;  
A:Experimental source: clone F41E7  
C:Genetics:  
A:Gene: CESP:F41E7.3  
A:Map position: X  
A:Introns: 76/2; 161/3; 220/3; 279/2; 325/2; 350/1; 378/1  
C:Superfamily: neurokinin 1 receptor  
Query Match 20.2%; Score 419.5; DB 2; Length 412;  
Best Local Similarity 29.4%; Pred. No. 5.6e-28;  
Matches 101; Conservative 72; Mismatches 94; Indels 77; Gaps 13;  
QY 53 YIRSIPTFLYGLFVLGIFGN-----GGVLWAVARNKRLQSAARNVFL 95  
Db 5 YFRPFISYCAVFLVASSGNFLVSNIIIDFSSFTTVPFKVVVWVWTKRMQITNIFIT 64  
QY 96 NILFTDLILVFTPAVTPPYAMTKDWAFGSMCHLVPL-----SN--S 136  
Db 65 NLAUSDIMVNTSLMLTPTTYSIGHWIFGGGLCHGLPLFQGIHLHDGKLSDDQASNYTG 124  
QY 137 CSVFTVTSLSLTSLDKP-----LHINDPTKQPSVIRQALAITELIWIIVSTLINLP 187  
Db 125 TSIFISTWLTALIDRYIVIVHNSNININD-----RMSRCLSTFVLIVMLQSLLLVTP 180  
QY 188 YL-----MSFEHVDGSPYVQGETPYCGHFCDEANQSENRSKIYGTVMMLQVFPVMAVI 243  
Db 181 YAINMKLNIHPCDFLI-----CSB-DMSNAEFSIFGIVVMILQFILPFLVLI 228  
QY 244 TYCYPKILOKVKDMIIQNAQFCOSLTQKQSDATSRKKKNVILIAMVVTPIGCVLPT 303  
Db 229 AISYIKI-----WLFNLSR--QSMTER-KSD-IRKCKRLRLMLVVMVVIPIACWFFPN 277  
QY 304 LNLVKDPKPEWELKRPQFFWAINAHVIAVMSLVVNPFLFWL 347  
Db 278 LNLCLRLDKLD-NFRMGYSFVFLSVHLSMTATAWNPLIYAFM 320  
RESULT 6  
T24487  
hypothetical protein T05A1.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T24487  
R:Lloyd, C.  
submitted to the EMBL Data Library, December 1995  
A:Reference number: Z19897  
A:Accession: T24487  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-373 <WIL>  
A:Cross-references: UNIPROT:Q22188; UNIPARC:UPI00001641C3; EMBL:Z68219; PIDN:CAA92481.1;  
A:Experimental source: clone T05A1

C:Genetics:  
A:Gene: CESP:T05A1.1  
A:Map position: 4  
A:Introns: 48/2; 106/3; 219/2; 254/1; 280/1; 309/1; 327/2  
Query Match 18.7%; Score 387.5; DB 2; Length 373;  
Best Local Similarity 30.6%; Pred. No. 2.6e-25;  
Matches 89; Conservative 69; Mismatches 98; Indels 35; Gaps 8;  
QY 47 DITVDPIRISIFTFLYGLFVLGIFGNCGVLWAVARNKRLQSAARNVFLNLIFTDLILVF 106  
Db 18 DMTNEPTVLVTSLSLYLHIFLGLGNSAVLYLTKHROLOTVQNIIFILNCASVLMCL 77  
QY 107 TAIPTVTPYAMTKDWAFGSMCHLVPLNSCSVFVTSMSLTASISLDKFLHINDPTKQPV 166  
Db 78 TSLPITFITNVYKQWFFSFPVCKLIPVQASIFVSTFSLSAIALDRYNLVVRPHKQKLS 137  
QY 167 IQCALAITFLIWIIVSTLINLPV--LMSFEHVDGSPYVQGETPYCGHFCDEANQSENRS 224  
Db 138 SRSAAMIALIWIISVVVCMPIGYTNDVEKLG-----LCGEYCSE-HWPLAEVR 186  
QY 225 KIYGTVMMLQVFPVMAVITYCYFKI-----LOKVS-KDMIIQNAQFCOSLTQK 272  
Db 187 KGYTFLVLITQLFPFPAWAFYNYIFSLRQRVETKCLKLSERQLLENSTTCGTNHI 246  
QY 273 QRSDATSRKKKNVILIAMVVTPIGCVLPTLINL--VKDPKKEPEWELKRP 321  
Db 247 VSNIAVSK-----GHIVYQGNNTF---LEITFLNVFFVLMYSSSKWKGK 289  
RESULT 7  
T19186  
hypothetical protein C10C6.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T19186  
R:White, S.  
submitted to the EMBL Data Library, December 1996  
A:Reference number: Z19086  
A:Accession: T19186  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-376 <WIL>  
A:Cross-references: UNIPROT:P90745; UNIPARC:UPI000003C14C; EMBL:Z83217; PIDN:CA805681.1;  
A:Experimental source: clone C10C6  
C:Genetics:  
A:Gene: CESP:C10C6.2  
A:Map position: 4  
A:Introns: 54/3; 105/3; 133/3; 179/2; 251/2; 348/3  
C:Superfamily: neurokinin 1 receptor  
Query Match 18.4%; Score 382; DB 2; Length 376;  
Best Local Similarity 28.7%; Pred. No. 7.8e-25;  
Matches 92; Conservative 78; Mismatches 127; Indels 24; Gaps 9;  
QY 54 IRSIFTFLYGLFVLGIFGNCGVLWAVARNKRLQSAARNVFLNLIFTDLILVFTPAVTP 113  
Db 24 IRAIFSLLYLLVWGAIVGNTLVYLTFTFNQVSLSVRTVFGCLAGSDLLMCLFSLPITA 83  
QY 114 WYAMTKDWAFGSMCHLVPLNSCSVFVTSMSLTASISLDKFLHINDPTKQPVIRQALAI 173  
Db 84 ISIFSRVWVFPALFKLIGVFGGTFIVSSFTLTVALDRCVLILRPQEIYVFPRAVEI 143  
QY 174 TFLIWIIVSTLINLPVMSFEHVDGSPYVQGETPYCGHFCDEANQSENRS-----RKI 226  
Db 144 VFCIWLGLYSLALPGVI---YSDIAVDE-----ICGTFCEE-NWPDFNPTGRSGIRRA 194  
QY 227 YGTTVMMLQVFPVMAVITYCYFKILOKVKDMIIQNAQFCOSLTQKQSDATSRKKKNV 286  
Db 195 YGLSVLVLPQFGIPALISSICYW-MISRVMSDQARRRG--HNIRSESETKLVNRKTRNR 251  
QY 287 ILIAMVVTPIGCVLPTLINLVKDPKKEPEWELKRPQFFWAINAHVIAVMSLVVNPFLFW 346

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Db 252 MMIVVVVGVFLAMPFNANVLYRDLFGISKWYST---VPAL-CHVCAMCSAVLNPIIYSW 307
Qy 347 LTRKQKSGLSKILNSTGSK 367
Db 308 F-NPQFRQSITTLFGTDEAR 327

RESULT 8
152315
G protein-coupled receptor UHR-1 - rat
C:Species: Rattus sp. (rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-May-2000
C:Accession: I52315
R:Welch, S.K.; O'Hara, B.F.; Kilduff, T.S.; Heller, H.C.
Biochem. Biophys. Res. Commun. 209, 606-613, 1995
A:Title: Sequence and tissue distribution of a candidate G-coupled receptor cloned from
A:Reference number: I52315; MUID:95251659; PMID:7733930
A:Accession: I52315
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-370 <RES>
A:Cross-references: UNIPARC:UPI000004B9B3; GB:S77867; NID:g998527; PIDN:AAB34129.1; PID:
C:Superfamily: neurokinin 1 receptor

Query Match 18.0%; Score 373.5; DB 1; Length 370;
Best Local Similarity 26.7%; Pred. No. 4.1e-24;
Matches 93; Conservative 80; Mismatches 154; Indels 21; Gaps 8;

Qy 18 STISNVTSHNSGSCIQIAEALAAQGIIDDITVDFYIRSIFTLFGFLVILGIFGNGVL 77
Db 23 STPAQSAESESNSVATVPRAAAVTPQSGLVHQLGLVNLVSVVVVGLVGNCLV 82
Qy 78 WAVARNKQLQARNVFLNLFTDLILVFTAIPTVPTWAM-TKDWAFGSVVMCHLVPLSNS 136
Db 83 LVIAVRRLHVNFTNLGNLALSDVLMCAACVPLTLAYAFPRGVFGGGLCHLVFFLQP 142
Qy 137 CSVPVTSKSLTAISDKFLHNDPTKQPSVIRQALAITFLIWIIVSTLINLPLVMSFEVD 196
Db 143 VTVVSVFTLTIAVDRIIVLVHPURRISKLSAYAVGLWALSVALPAAVTYHYE 202
Qy 197 GSFYVQGPETPCYGHFCDENMQS-ENSRKIYGTVMLLQFVVPNAVITYCYFKILQVS 255
Db 203 ----LKPHDVLRCDF-----WGSQRQRIYAWGLLGTLLPLAILLSVVRVSK-- 251
Qy 256 KDMITQNAQFCOSLTQKQRSDATSKKKVNYILIAMVVTFCGWLPLTLLMLVKDFKKEP 315
Db 252 ----LNRNVVPGSVTQSOADMRRRRRTFCLLVVVVVVFALCWLPLHFNLLRDL--DP 305
Qy 316 EWLKRPPE-FWAINAHVIAMSLVVWNPLLFPWLTRKQKSGLSKILNS 362
Db 306 RAIDPYAFGLVQLLCHWLAMSACTNPFYIAML-HDSFRELRRMLLS 352

RESULT 9
863685
neuropeptide Y receptor D type - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S63685
R:Gregor, P.; Millham, M.L.; Feng, Y.; DeCarr, L.B.; McCaleb, M.L.; Cornfield, L.J.
FEBS Lett. 381, 58-62, 1996
A:Title: Cloning and characterization of a novel receptor to pancreatic polypeptide, a n
A:Reference number: S63685; MUID:96193913; PMID:8641440
A:Accession: S63685
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-375 <GR>
A:Cross-references: UNIPROT:Q61041; UNIPARC:UPI0000027CC7; EMBL:U40189; NID:g1223969; PI
C:Superfamily: neurokinin 1 receptor

Query Match 17.1%; Score 354; DB 2; Length 375;
Best Local Similarity 25.7%; Pred. No. 1.9e-22;
Matches 103; Conservative 74; Mismatches 142; Indels 82; Gaps 12;
```

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Qy 21 SNVITSHN-NGSCIQIAEALAAQGIIDDITVDFYIRSIFTLFGFLVILGIFGNGVLWA 79
Db 21 TNPLDSPYFNFDGQDSAEELA-----FIIT-----YSIEILGVGLNCLIFV 65
Qy 80 VARNKQLQARNVFLNLFTDLILVFTAIPTVPTWAMTKDWAFGSVVMCHLVPLSNSCSV 139
Db 66 TTRQKEKSNVTNLLIANLAFSDFLMCLICQLPTVTVTMDVWIRGEVLCKMLTFIQMSV 125
Qy 140 FVTSWSLTAISDKFLHNDPTKQPSVIRQALAITFLIWIIVSTLINLPLVMS-----PEH 194
Db 126 TVSILSLVLVALERHQLIINPTGKPSIFQAYLGIWVIFWISCFSLSPFLANSTLNDLFH 185
Qy 195 VDGSFYVQGPETPCYGHFCDENMQS-ENSRKIYGTVMLLQFVVPNAVITYCYFK 249
Db 186 YNHSKVVE-----FLEDKVVCFVSWSDHRLIYTTFLLLFQVCIPAFILVCYIR 236
Qy 250 ILQKVSMDIITQNAQFCOSLTQKQRSDATSKKKVNYILIAMVVTFCGWLPLTLLMLVK 309
Db 237 IYQRLQKQKHVFHAHAC-----SSRAGQMKRINSLMTMTVTAFAVLWPLHVFNTLE 288
Qy 310 DFKEPEPWLKRPFPFWAINA-----HVIAMSLVWNPPLFPWLTRKQKSGLSKI 359
Db 289 DWYQGE-----AIPACHGNLIPLMCHLLAMASTCVNPFYIGFLNINFKKDIKALV 337
Qy 360 L-----NSTEGSKAGGSLGRIGLHDLPTST-HSDRCAGN 395
Db 338 LTCHRSFQGES-----EHLPLSTVHIDLSKGS 365

RESULT 10
A45490
neuropeptide Y/peptide YY receptor Y1 - human
C:Species: Homo sapiens (man)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A45490; A46133; A42773
R:Herzog, H.; Baumgartner, M.; Vivero, C.; Selbie, L.A.; Auer, B.; Shine, J.
J. Biol. Chem. 268, 6703-6707, 1993
A:Title: Genomic organization, localization, and allelic differences in the gene for the
A:Reference number: A45490; MUID:93203272; PMID:8095935
A:Accession: A45490
A:Molecule type: DNA
A:Residues: 1-384 <HER>
A:Cross-references: UNIPROT:P25929; UNIPARC:UPI000002D509; GB:L07615; NID:g189284; PIDN:
A>Note: sequence extracted from NCBI backbone (NCBIN:128005, NCBI:P:128000)
R:Herzog, H.; Hort, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992
A:Title: Cloned human neuropeptide Y receptor couples to two different second messenger
A:Reference number: A46133; MUID:92335184; PMID:1321422
A:Accession: A46133
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-384 <HE2>
A:Cross-references: UNIPARC:UPI000002D509
A>Note: sequence extracted from NCBI backbone (NCBI:P:108538)
R:Larhammar, D.; Blomqvist, A.G.; Yee, F.; Jazin, E.; Yoo, H.; Wahlested, C.
J. Biol. Chem. 267, 10935-10938, 1992
A:Title: Cloning and functional expression of a human neuropeptide Y/peptide YY receptor
A:Reference number: A42773; MUID:92283782; PMID:13117848
A:Accession: A42773
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-384 <LAS>
A:Cross-references: UNIPARC:UPI000002D509; GB:M88461; NID:g189155; PIDN:AAA73215.1; PID:
A:Experimental source: fetal brain
A>Note: sequence extracted from NCBI backbone (NCBIN:104735, NCBI:P:104736)
C:Genetics:
A:Gene: GDB:NPY1R; NPYR
A:Cross-references: GDB:132643; OMIM:162641
A:Map position: 4q31.3-q32
C:Superfamily: neurokinin 1 receptor
C:Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thiolester
P:37-66/Domain: transmembrane #status predicted <TM1>
```



F;77-103/Domain: transmembrane #status predicted <TM2>  
F;118-136/Domain: transmembrane #status predicted <TM3>  
F;155-179/Domain: transmembrane #status predicted <TM3>  
F;209-232/Domain: transmembrane #status predicted <TM5>  
F;261-286/Domain: transmembrane #status predicted <TM6>  
F;300-323/Domain: transmembrane #status predicted <TM6>  
F;113-198/Disulfide bonds: #status predicted  
F;186/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;338/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 16.7%; Score 346.5; DB 2; Length 384;  
Best Local Similarity 25.7%; Pred. No. 8.4e-22;  
Matches 88; Conservative 78; Mismatches 154; Indels 23; Gaps 6;

QY 18 STISNVITSHNNGSCIQIABAAQAGIDITVDYFIRSIPTFLYGLFVILFGNGVL 77  
DB 3 STLFQVNHNSVHSFSEKQAQLAFENDCHLPALAIPTLALAYGAVIILGVSGNLALI 62  
QY 78 WAVARNKRLQSRNVFLNLIFTDLLVFTAIPTVTPYAMTKDWAQSVNCHLVPLNSC 137  
DB 63 IILKQKEMVNTNIIIVNLSFSDLLVAINMCLPFTFYITLMDHWVFGAACKLNPFVQC 122  
QY 138 SVFVTSWSTALSLDKFLHNDTPKQVSIROALAITFLIWIIVSTLINLPYL----- 190  
DB 123 SITVSIFSLVLIIVERHQLINRGWRPNRHHAYVGLAVIWLAVASSLPFLIYQWTD 182  
QY 191 SFPHVGSFVQGETPYCGHFCDEANQSENKRKYITVTMLLQFVVPMAVITYCYFKI 250  
DB 183 PFQNVTLDAYKDK-----YVCFD-QFPSDSHRLSYTLLLVLLQVFGPLCFIFCYFKI 234  
QY 251 LQKVSXDMIIQNAQFCQSLTKORSDATSKKKVYILIAMVTFVTCMLPLTLNLVKD 310  
DB 235 YIRLKR-----RNNMDKRDNKVRSSET---KRNIMLLSIVVAFVAVCMLEFLTIFNTVFD 287  
QY 311 FKPEWLKRQPPFWMAINAHVIAVSLVWNPLLFWMLTRQKR 353  
DB 288 WNHQIATCNHNLFL-CHLTAMISTCVNPIFYGLNKNFQR 329

RESULT 11  
S27388  
neuropeptide Y receptor NPY-1 - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S27388  
R:Eva, C.; Oberlo, A.; Sprengel, R.; Genazzani, E.  
FEBS Lett. 314, 285-288, 1992  
A:Title: The murine NPY-1 receptor gene. Structure and delineation of tissue-specific exons  
A:Reference number: S27388; MUID:93106169; PMID:1468559  
A:Accession: S27388  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-382 <EVA>  
A:Cross-references: UNIPROT:Q04573; UNIPARC:UPI0000024A23; EMBL:Z18280; NID:G53438; PIDN  
C:Superfamily: neurokinin 1 receptor

Query Match 16.5%; Score 342; DB 2; Length 382;  
Best Local Similarity 25.6%; Pred. No. 2e-21;  
Matches 87; Conservative 80; Mismatches 155; Indels 18; Gaps 6;

QY 18 STISNVITSHNNGSCIQIABAAQAGIDITVDYFIRSIPTFLYGLFVILFGNGVL 77  
DB 3 STLFQVNHNSVHSFSEKQAQLAFENDCHLPALAIPTLALAYGAVIILGVSGNLALI 61  
QY 78 WAVARNKRLQSRNVFLNLIFTDLLVFTAIPTVTPYAMTKDWAQSVNCHLVPLNSC 137  
DB 62 IILKQKEMVNTNIIIVNLSFSDLLVAVMCLPFTFYITLMDHWVFGAACKLNPFVQC 121  
QY 138 SVFVTSWSTALSLDKFLHNDTPKQVSIROALAITFLIWIIVSTLINLPYLMSFEHVDG 197  
DB 122 SITVSIFSLVLIIVERHQLINRGWRPNRHHAYIGITVIWLAVASSLPFVIYQILTD- 180  
QY 198 SFVQVGETPYCGHFCDE-----ANQSENKRKYITVTMLLQFVVPMAVITYCYFKLOK 253

DB 181 ----EPQNVSLAAPKDKVCFDKPSPDSHRLSYTLLLVLLQYFGPLCFIFCYFKIYR 236  
QY 254 VSKDMIIQNAQFCQSLTKORSDATSKKKVYILIAMVTFVTCMLPLTLNLVKDFKK 313  
DB 237 LKR-----RNNMDKIRDYSRSET---KRNIMLLSIVVAFVAVCMLEFLTIFNTVPDWNH 289  
QY 314 EPWLKRQPPFWMAINAHVIAVSLVWNPLLFWMLTRQKR 353  
DB 290 QIIATCNHNLFL-CHLTAMISTCVNPIFYGLNKNFQR 328

## RESULT 12

A41738  
neuropeptide Y receptor - fruit fly (Drosophila melanogaster)  
N:Alternate names: G protein-coupled receptor PR4  
C:Species: Drosophila melanogaster  
C>Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 09-Jul-2004  
C:Accession: A41738  
R:Li, X.J.; Wu, Y.N.; North, R.A.; Forte, M.  
J. Biol. Chem. 267, 9-12, 1992  
A:Title: Cloning, functional expression, and developmental regulation of a neuropeptide  
A:Reference number: A41738; MUID:92112730; PMID:1370455  
A:Accession: A41738  
A:Molecule type: mRNA  
A:Residues: 1-449 <LIA>  
A:Cross-references: UNIPROT:P25931; UNIPARC:UPI0000130B36; GB:M81490; NID:G157996; PIDN  
C:Genetics:  
A:Gene: FlyBase:NepYr  
A:Cross-references: FlyBase:FBN0004842  
C:Superfamily: neurokinin 1 receptor  
C:Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 16.2%; Score 337; DB 2; Length 449;  
Best Local Similarity 27.0%; Pred. No. 6.5e-21;

Matches 88; Conservative 75; Mismatches 145; Indels 18; Gaps 10;  
QY 46 DDITVDYFIRSIPTFLYGLFVILFGNGVILWAVARNKRLQSRNVFLNLIFTDLILV 105  
DB 81 EDWSSAYFKIIVYLYIFIFALINGTVCVIVVTPRMTVTNVTYASLAIGDILMS 140  
QY 106 FTAIPVTPYAM--TKDWAQSVNCHLVPLNSCSVFTVTSWSTALSLDKFLHNDTPKQ 163  
DB 141 FPCBP-SSPFIILNYPFGALCHLVNYSQAVSLVSAYTLVAISIDRYIAIMPLKP 199  
QY 164 PVSIRQALAITFLIWIIVSTLINLPYLMSFEHVDG-SFYVQGETPYCGHFCDEANQSEN 222  
DB 200 RITKYATVFIAGVFIATATLPIPI-----VSGLDIPMSPWHTKCEKICREM-WPSRS 254  
QY 223 SRKIYGTVMMLQFVVPMAVITYCYFKILOKYSKDMIQNAQFCQSLTKORSDATSRKK 282  
DB 255 QBYVYVTLSEFALQFVVPVGLVIFTYARITIRVWAKRPPGEA-----TNRDQRMARSKRK 309  
QY 283 KNYVILIAMVTFVTCMLPLTLNLVKDFKPEWLMKROPFFWAINAHVIAVSLVWNPL 342  
DB 310 MYK-WMLTVIVFTCTCMLPFNLIQLLNDDEFAHW-DPLPYVW-FAFHWLAMSCHCCNPI 366

QY 343 LFFWLMTRKQKRGSLKILNSTEGSKK 368  
DB 367 IYCYNNAR-FRSGFVQLMRMPLGR 391

## RESULT 13

S12863

G protein-coupled receptor FC5 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004  
C:Accession: S12863; S19101  
R:Eva, C.; Keinaenen, K.; Monyer, H.; Seeburg, P.; Sprengel, R.  
FEBS Lett. 271, 81-84, 1990  
A:Title: Molecular cloning of a novel G protein-coupled receptor that may belong to the  
A:Reference number: S12863; MUID:91032093; PMID:2172008  
A:Accession: S12863



F:342/Binding site: palmitate (Cys) (covalent) #status predicted  
F:372/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.6% Score 324; DB 2; Length 381;  
Best Local Similarity 25.5%; Pred. No. 6.9e-20;  
Matches 91; Conservative 67; Mismatches 139; Indels 60; Gaps 9;

QY	37	AEAIAGGIDDIIVDFY-----IRSIFLYGFLFVLGI	70
Db	6	AEADENQTVEEKVQYGFQTPRGELVPDPPELIDSTKLEIVQVVLILAYCSIIILGV	65
QY	71	FGNGGYLWAVARNKRQARNVFLNLIFTDLILVFTAIPTVPWYAMTKDWAFGSVMCHL	130
Db	66	IGNSLVHVVIKPKSMRTVTNPFIANLAVADLLVNTLCIFPFTLYTILMGWQGPVICHL	125
QY	131	VFLNSCSVFTVTSWLSLTAISLDFLHNDPTKQPSIROALAITFLIMIVSTLINLPYLM	190
Db	126	VPYAQGLAVQVSTITLTIALDRHRCIVVHLESKISKRISFLIIGLAWGISALLASPLAI	185
QY	191	SFEH----VDGSFYVQGETPYCGHFCDEANQSENRSKIYGT-----TVMLLQFVVVPMAY	242
Db	186	FREYSLIEIIPDFEIVA-----CTE-KWPGE-EKSIYGTVYSLSLLLIYVVLPLGI	234
QY	243	ITYCYFKILQVSKDMI--IQNAQCQSLTKQSDATSRKKKNVYILIAMVVTFTIGCWL	300
Db	235	ISFSYTRISWKLKNHVSFGAANDHYHQ-----RRKTTYKMLVCVVVVFAVSWL	282
QY	301	PLTLNLNVKDFKKBPFWLKRQPPFWAINAHVIAVWVNVNPLLPFLWLRKQKRSGLS	357
Db	283	PLHAFQLAVDIDSQVLDLKEYKLIPTV-FHIIAMCSTFANPLLYGMWNSNYRKAFLS	338

Search completed: May 8, 2006, 09:34:15  
Job time : 42 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 8, 2006, 09:26:17 ; Search time 187 Seconds  
(without alignments)  
932.799 Million cell updates/sec

Title: US-10-650-467-105

Perfect score: 2074

Sequence: 1 WYSSAATISTITTPSTI.....QLHLLPTSTHSRDCAGNSF 397

Scoring table: BLOSUM62

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_21.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2074	100.0	397	AAU03851	Aau03851 G protein
2	2074	100.0	499	AAU03820	Aau03820 G protein
3	1899	91.6	433	AAU03852	Aau03852 G protein
4	607.5	29.3	450	AAU03809	Aau03809 G protein
5	607.5	29.3	539	AAU03809	Aau03809 G protein
6	529	25.5	518	AAU03855	Adn23955 Bacterial
7	529	25.5	600	AAU03855	Adn23955 Bacterial
8	529	25.5	600	AAU03855	Adn23955 Bacterial
9	529	25.5	600	AAU03855	Adn23955 Bacterial
10	529	25.5	600	AAU03855	Adn23955 Bacterial
11	529	25.5	600	AAU03855	Adn23955 Bacterial
12	529	25.5	600	AAU03855	Adn23955 Bacterial
13	521	25.1	600	AAU03855	Adn23955 Bacterial
14	515.5	24.9	376	AAU03811	Adn4524 Fruit fly
15	514	24.8	374	AAU03811	Adn4524 Fruit fly
16	485.5	23.4	457	AAU03813	Adn24291 Bacterial
17	485.5	23.4	457	AAU03813	Adn24291 Bacterial
18	461.5	22.3	365	AAU03818	Adn24116 Bacterial
19	461.5	22.3	365	AAU03818	Adn24116 Bacterial
20	460.5	22.2	387	AAU03808	Adn24305 Bacterial
21	458	22.1	381	AAU03807	Adn24305 Bacterial
22	458	22.1	402	AAU03805	Aau03807 G protein
23	458	22.1	404	AAU03804	Aau03805 G protein
24	458	22.1	406	AAU03806	Aau03804 G protein

25	419.5	20.2	412	8	ADN24230	Adn24230 Bacterial
26	390.5	18.8	375	6	ABG73520	Abg73520 D. rerio
27	388	18.7	458	4	AAU03207	Aau03207 Fruit fly
28	388	18.7	458	7	ADL83376	Adl83376 Drosophil
29	388	18.7	458	8	ADL83376	Adl83376 Drosophil
30	388	18.7	458	9	ADV91976	Adv91976 DmGPCR2b
31	387.5	18.7	373	8	ADN23444	Adn23444 Bacterial
32	386.5	18.6	370	8	ADO29366	Ado29366 Mouse GPC
33	386.5	18.6	380	2	AAW27510	Aaw27510 Consensus
34	386	18.6	370	2	AAW27510	Aaw27510 Human pit
35	386	18.6	370	2	AAW31379	Aaw31379 Human G p
36	386	18.6	370	2	AAW95181	Aaw95181 Human G-p
37	386	18.6	370	2	AAW97221	Aaw97221 Human pit
38	386	18.6	370	4	ABG62539	Abg62539 Human CRH
39	386	18.6	370	6	ABP81880	Abp81880 Human G p
40	386	18.6	370	8	ADO29365	Ado29365 Human GPC
41	386	18.6	370	8	ADT98602	Adt98602 Human wil
42	385.5	18.6	370	3	AAV87503	Aav87503 Murine G
43	385.5	18.6	370	4	AAW67653	Aaw67653 Amino aci
44	382	18.4	370	3	AAV87505	Aav87505 Human G c
45	382	18.4	376	4	AAU03822	Aau03822 G protein

## ALIGNMENTS

### RESULT 1

AAU03851

ID AAU03851 standard; protein; 397 AA.

XX AC AAU03851;

XX DT 12-SEP-2001 (first entry)

XX DE G protein-coupled receptor-like (GPCR-like) receptor protein #23.

XX DE G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;

KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;

KW neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;

KW fruitfly.

XX OS Homo sapiens.

XX PN WO200138533-A2.

XX PD 31-MAY-2001.

XX PF 24-NOV-2000; 2000WO-US032225.

XX PR 24-NOV-1999; 99US-0167523P.

XX (PHAA ) PHARMACIA & UPJOHN.

XX PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;

XX DR WPI; 2001-343952/36.

XX N-PSDB; AAS07253.

XX Using G-protein-coupled receptor (GPCR)-like receptors to identify

PT candidate compounds for the treatment and prevention of invertebrate

PT parasites, especially helminths and insects.

XX Claim 6; Page 175-176; 219pp; English.

XX The sequence represents a G protein-coupled receptor-like (GPCR-like)

CC receptor protein. GPCR-like receptors and their associated nucleic acids

CC may be used to identify candidate compounds for their ability to modulate

CC the activity of GPCRs. The sequences therefore are useful for treating

CC parasites, especially helminths and insects, and particularly ailments

CC related to aberrant neurological and neuromuscular function

XX Sequence 397 AA;

XX

```
Query Match      100.0%; Score 2074; DB 4; Length 397;
Best Local Similarity 100.0%; Pred. No. 4.5e-209;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVSSAATISTITSTTTTPSTISNVITSHNNGSCIOIAEAAQAGIDDDITVDYFIRSIFTF 60
DB 1 MVSSAATISTITSTTTTPSTISNVITSHNNGSCIOIAEAAQAGIDDDITVDYFIRSIFTF 60

QY 61 LYGLFVLGIFGNGGVLMAVARNKRLQSAARNVFLNLIFTDLILVFTTAIPVTPMYAMTKD 120
DB 61 LYGLFVLGIFGNGGVLMAVARNKRLQSAARNVFLNLIFTDLILVFTTAIPVTPMYAMTKD 120

QY 121 WAFGVMCHLVPLNSCSVFVTSWLSLTAISLDKFLHNDPTKQPVSIROALAITFLIIV 180
DB 121 WAFGVMCHLVPLNSCSVFVTSWLSLTAISLDKFLHNDPTKQPVSIROALAITFLIIV 180

QY 121 WAFGVMCHLVPLNSCSVFVTSWLSLTAISLDKFLHNDPTKQPVSIROALAITFLIIV 180
DB 121 WAFGVMCHLVPLNSCSVFVTSWLSLTAISLDKFLHNDPTKQPVSIROALAITFLIIV 180

QY 181 STLINLPYLMSFEHVDGSFYVQGETPYCGHFCDEANWQSENRSKIYGTVMLLQFVVVPM 240
DB 181 STLINLPYLMSFEHVDGSFYVQGETPYCGHFCDEANWQSENRSKIYGTVMLLQFVVVPM 240

QY 241 AVITYCYFKILQKVSQKMIQNAQFCQSLTQKQSDATSRKKKNYILIAMVVTFIGCWL 300
DB 241 AVITYCYFKILQKVSQKMIQNAQFCQSLTQKQSDATSRKKKNYILIAMVVTFIGCWL 300

QY 301 PLTLNLVKDPKKEPEWLKQPPFWAINAHVIAVMSLVVWNPFLFPWLTRKQKRSGLSKIL 360
DB 301 PLTLNLVKDPKKEPEWLKQPPFWAINAHVIAVMSLVVWNPFLFPWLTRKQKRSGLSKIL 360

QY 361 NSTEGSKAGGGLRGILQHLDLPTSTHSDRCAGNSP 397
DB 361 NSTEGSKAGGGLRGILQHLDLPTSTHSDRCAGNSP 397

RESULT 2
AAU03820
ID AAU03820 standard; protein; 499 AA.
XX
XX AAU03820;
XX
DT 12-SEP-2001 (first entry)
XX
DE G protein-coupled receptor-like (GPCR-like) receptor protein #19.
XX
KW G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
KW neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;
KW fruitfly.
XX
OS Homo sapiens.
XX
PN WO200138533-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-US032225.
XX
PR 24-NOV-1999; 99US-0167523P.
XX
PA (PHAA ) PHARMACIA & UPJOHN.
XX
PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;
XX
DR WPI; 2001-343952/36.
XX
DR N-PSDB; AAS07219.
XX
PT Using G-protein-coupled receptor (GPCR)-like receptors to identify
PT candidate compounds for the treatment and prevention of invertebrate
PT parasites, especially helminths and insects.
XX
PS Claim 6; Page 147-149; 219pp; English.
XX
XX The sequence represents a G protein-coupled receptor-like (GPCR-like)

CC receptor protein. GPCR-like receptors and their associated nucleic acids
CC may be used to identify candidate compounds for their ability to modulate
CC the activity of GPCRs. The sequences therefore are useful for treating
CC and preventing infection by endoparasitic and ectoparasitic invertebrate
CC parasites, especially helminths and insects, and particularly ailments
CC related to aberrant neurological and neuromuscular function
XX
XX Sequence 499 AA;
XX
Query Match      100.0%; Score 2074; DB 4; Length 499;
Best Local Similarity 100.0%; Pred. No. 6.2e-209;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVSSAATISTITSTTTTPSTISNVITSHNNGSCIOIAEAAQAGIDDDITVDYFIRSIFTF 60
DB 103 MVSSAATISTITSTTTTPSTISNVITSHNNGSCIOIAEAAQAGIDDDITVDYFIRSIFTF 162

QY 61 LYGLFVLGIFGNGGVLMAVARNKRLQSAARNVFLNLIFTDLILVFTTAIPVTPMYAMTKD 120
DB 163 LYGLFVLGIFGNGGVLMAVARNKRLQSAARNVFLNLIFTDLILVFTTAIPVTPMYAMTKD 222

QY 121 WAFGVMCHLVPLNSCSVFVTSWLSLTAISLDKFLHNDPTKQPVSIROALAITFLIIV 180
DB 223 WAFGVMCHLVPLNSCSVFVTSWLSLTAISLDKFLHNDPTKQPVSIROALAITFLIIV 282

QY 181 STLINLPYLMSFEHVDGSFYVQGETPYCGHFCDEANWQSENRSKIYGTVMLLQFVVVPM 240
DB 283 STLINLPYLMSFEHVDGSFYVQGETPYCGHFCDEANWQSENRSKIYGTVMLLQFVVVPM 342

QY 241 AVITYCYFKILQKVSQKMIQNAQFCQSLTQKQSDATSRKKKNYILIAMVVTFIGCWL 300
DB 343 AVITYCYFKILQKVSQKMIQNAQFCQSLTQKQSDATSRKKKNYILIAMVVTFIGCWL 402

QY 301 PLTLNLVKDPKKEPEWLKQPPFWAINAHVIAVMSLVVWNPFLFPWLTRKQKRSGLSKIL 360
DB 403 PLTLNLVKDPKKEPEWLKQPPFWAINAHVIAVMSLVVWNPFLFPWLTRKQKRSGLSKIL 462

QY 361 NSTEGSKAGGGLRGILQHLDLPTSTHSDRCAGNSP 397
DB 463 NSTEGSKAGGGLRGILQHLDLPTSTHSDRCAGNSP 499

RESULT 3
AAU03852
ID AAU03852 standard; protein; 433 AA.
XX
XX AAU03852;
XX
DT 12-SEP-2001 (first entry)
XX
DE G protein-coupled receptor-like (GPCR-like) receptor protein #24.
XX
KW G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
KW neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;
KW fruitfly.
XX
OS Homo sapiens.
XX
PN WO200138533-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-US032225.
XX
PR 24-NOV-1999; 99US-0167523P.
XX
PA (PHAA ) PHARMACIA & UPJOHN.
XX
PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;
XX
DR WPI; 2001-343952/36.
DR N-PSDB; AAS07254.
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XX FN US2003233675-A1.
XX PD 18-DEC-2003.
XX PF 20-FEB-2003; 2003US-00369493.
XX PR 21-FEB-2002; 2002US-0360039P.
XX PA (CAOY/) CAO Y.
XX PA (HINK/) HINKLE G J.
XX PA (SLAT/) SLATER S C.
XX PA (CHEN/) CHEN X.
XX PA (GOLD/) GOLDMAN B S.
XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WI MPI; 2004-061375/06.
XX DR
XX XX New recombinant DNA construct comprising a promoter positioned to provide
XX FT for expression of a polynucleotide encoding a polypeptide from a
XX FT microbial source, useful for producing plants with improved properties.
XX XX
XX PS Claim 1; SEQ ID NO 6608; 122pp; English.
XX CC
XX CC The invention relates to a recombinant DNA construct comprising a
XX CC promoter functional in a plant cell, where the promoter is positioned to
XX CC provide for expression of a polynucleotide encoding a polypeptide from a
XX CC microbial source. The invention also relates to a transformed plant
XX CC comprising the recombinant DNA construct and a method of producing a
XX CC transformed plant having an improved property. The plant is a crop plant
XX CC such as maize or soybean. The method of producing a transformed plant
XX CC having an improved property comprises transforming a plant with the
XX CC recombinant DNA construct and growing the transformed plant, where the
XX CC polynucleotide or polypeptide is useful for improving plant properties.
XX CC The recombinant DNA construct is useful for producing plants with
XX CC improved plant properties, e.g. improved cold, heat or drought tolerance,
XX CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX CC increased resistance to plant disease, better growth rate by modification
XX CC of the cell cycle pathway with plant growth regulators, increased rate of
XX CC homologous recombination, modified seed oil or protein yield and/or
XX CC content, improved yield by modification of carbohydrate, nitrogen or
XX CC phosphorus use and/or uptake, by modification of photosynthesis or by
XX CC providing improved plant growth and development under at least one stress
XX CC condition, improved lignin production or improved galactomannan
XX CC production. This sequence represents a bacterial polypeptide used in the
XX CC scope of the invention. Note: The sequence data for this patent did not
XX CC form part of the printed specification but was obtained in electronic
XX CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX XX
XX SQ Sequence 539 AA;
    Query Match 29.3%; Score 607.5; DB 8; Length 539;
    Best Local Similarity 35.3%; Pred. No. 1.8e-54;
    Matches 119; Conservative 76; Mismatches 111; Indels 31; Gaps 7;
QY 33 CTQIAEATAAQGIDITVDFTYRSTFTFLYGLFVLGIFGNGGVLWAVARNKRLQASRV 92
DB 9 CIDVNAIL--QQFNDVTFLFEVLGYSVLVFLIILGVLGNGLLITSLMRKKL-SVANI 65
QY 93 FLINLIPTDILVFTAIPTVPHYMTKDWAFGSMVCHLVPLNSGCVFTVTSMLTAISLD 152
DB 66 FLINLAVSLLLCITAVPTIPVLAQWIFGIMCKLVPTCOAFSEVLISLSLCYIAID 125
QY 153 KFLHNDPTKQPSVRSQALAIATFLIWTSLINLPLMSFEHVDGSGFYVQPGET----- 206
DB 126 YRSIVTFLRPSWSDHARWLLMFTVVAFLASYPL-----YYSQLKTMVENV 175
QY 207 FYCGHFCDBANQOSENRSKI-YGTTVMLLQFVVPMAVITYCFKILQKSKDMITQNAOF 265
DB 176 TLGCGFCGFBNQSDSEISKLTYSLLIQLIIPALINSFCYLMILQKVQTDWLVDGSM 235
QY 266 CQSLTQKQRSDATSRKKKVNILIAMVTFPGCWLPLTLNLVMDPKPEW----- 317

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Db 236 ---LTAQAQQAQTAVRKERVVYVLILMVLVFMACWFFPLSVAVNLPRDLGMRFEFCQTVYKVL 292
QY 318 LKRQPFPAWNAHVMIAVMSLVVWNPPLLFVWLRKQKRS 354
Db 293 MMDQMYEKLJNVHVIAVNTSIVMNPVLYFMNSKRRRA 329
RESULT 6
AAB86955
ID AAB86955 standard; protein; 518 AA.
XX AC AAB86955;
XX DT 11-DEC-2001 (first entry)
XX DE D. melanogaster peptide receptor SEQ ID 8.
XX KW Insect; fruitfly; peptide receptor; plant protection; insecticide.
XX OS Drosophila melanogaster.
XX PN DE10013618-A1.
XX PD 20-SEP-2001.
XX PF 18-MAR-2000; 2000DE-01013618.
XX PR 18-MAR-2000; 2000DE-01013618.
XX PA (PARB ) BAYER AG.
XX PI Antonicek H, Friedrich G, Schulte T;
XX WI MPI; 2001-571695/65.
XX DR N-PSDB; AAH49408.
XX XX New polypeptides from Drosophila melanogaster have biological activity of
XX FT peptide receptor, useful to find new compounds for plant protection and
XX FT insecticides.
XX PS Claim 2; Page 28-30; 128pp; German.
XX CC This invention describes novel polypeptides (PI) from Drosophila
XX CC melanogaster having the biological activity of a peptide receptor.
XX CC Molecules of the invention are used to find new plant protection
XX CC compounds or insecticides, or to find genes encoding a polypeptide
XX CC involved in the structure of functionally similar receptors in insects
XX CC This sequence represents a Drosophila melanogaster (fruitfly) peptide
XX CC receptor described in the method of the invention
XX SQ Sequence 518 AA;
    Query Match 25.5%; Score 529; DB 4; Length 518;
    Best Local Similarity 30.5%; Pred. No. 3.1e-46;
    Matches 136; Conservative 76; Mismatches 154; Indels 80; Gaps 12;
QY 6 ATISTISTTTPST-----ISNVITSHNNGSCQIAEATAAQSID----DITVDFY 53
DB 2 ANLSMLSTITTTSSSISTSQLPLVSTTNWLSLTPGTTSAILDVAASDEDRSGGIHQF 61
QY 54 IRSIFTFYGLFVLGIFGNGGVLWAVARNKRLQASRVFLINLIPTDILVFTAIPTVP 113
DB 62 VOIFPYFVIAVTVFVGFGVGVLCVVLNRNRAWQVTNIFITNLALSILLCLVAVPFTP 121
QY 114 WYATKDWAFGSMVCHLVPLNSGCVFTVTSMLTAISLDKFLHNDPTKQPSVRSQALAI 173
DB 122 LYTFMGRMAFGSLCHLVSAQCGSIYSTLTLSIAIDRYFVLIYPPHPRMKLSTCIGI 181
QY 174 FTLINIVSTLINLPLMSFE-----HVDGSGFYVQPG----- 204
DB 182 IVSIWVIALLATVPYGMVMTKMTNELVNGTGTNETLVLATLNLGNSFVAQSGFTEAPDS 241

```





G protein coupled receptor; DmGPCR1; DmGPCR1 binding partner; insect population control; ectoparasite; Alzheimer's disease; Parkinson's disease; Huntington's disease; neuromuscular disease; neurodegenerative disease; fruit fly; receptor.

Drosophila melanogaster.

US2003162223-A1.

28-AUG-2003.

30-OCT-2002; 2002US-00283423.

22-OCT-1999; 99US-00425676.

20-OCT-2000; 2000US-00693746.

06-AUG-2002; 2002US-00213821.

(LOWE/) LOWERY D E.

(SMIT/) SMITH V G.

(KUBI/) KUBIAK T M.

(LARS/) LARSEN M J.

Lowery DE, Smith VG, Kubiak TM, Larsen MJ;

WPI: 2003-897924/82.

N-PSDB; ADL83601.

Identifying a modulator of binding and/or function between a Drosophila melanogaster G protein coupled receptor and it's binding partner is useful to control insect populations and prevent or treat disease due to ectoparasites.

Disclosure; SEQ ID NO 2; 52pp; English.

The invention describes a method of identifying a modulator of binding and/or function between a Drosophila melanogaster G protein coupled receptor (DmGPCR1) and a DmGPCR1 binding partner, comprising contacting DmGPCR and the binding partner in the presence of a candidate compound and determining the effect of the compound on binding and/or function. Also described are: a method for controlling a population of insects; and a method of treating or preventing a disease or condition caused by an ectoparasite. The invention is used to control insects, particularly flies, ticks, fleas, lice, mites or cockroaches and to prevent or treat a disease caused by an ectoparasite, particularly Alzheimer's, Parkinson's, Huntington's disease and other neuromuscular and neurodegenerative diseases. This is the amino acid sequence of Drosophila melanogaster G protein coupled receptor 1 (DmGPCR1).

Sequence 600 AA;

Query Match 25.5%; Score 529; DB 7; Length 600;

Best Local Similarity 30.5%; Pred. No. 3.8e-46;

Matches 136; Conservative 76; Mismatches 154; Indels 80; Gaps 12;

6 ATISITSTTTTST-----ISNVITSHNGNSCICIAEAIQAQID---DITVDYF 53

2 ANLSWLSITTTTSSISSTSQLPLVSTTNWLSLSPGTTSAILDVAASDEDRSGGIHNOF 61

54 IRSITFLYGLFLGIFGNGVLMVAVARNKELQARNVFLNLIPTLILVTAIPVTP 113

62 VQIFPVLYATVFLGVFGVNLVCVVLNRAMQVTNIFITNLSLDILLCLVLPVTP 121

114 WTAMTKDWAFGVMCHVPLNSCSVFVTSWLSLTSLDKPLHINDPTKQPVSIQALAI 173

122 LYTFMGRWAFGRSLCHLVSFAQCISIYITSLTSLTAIDRYFVIYPPHPRKMLSTCIGI 181

174 TFLIVISTLINLPYLMSEF-----HVDGSFYVQPG----- 204

182 IVSIWIALLATVPYGMVMKMTNELVNGTGTNETLVEATLMNGSFVAQSGGFTEAPDS 241

205 -----ETPYCGHFCDEANWQNSRKIYGTWMLQFVVPMAVITVC 246

242 TSATQAYMQVMTAGTGTGPEMPVRYCEB-NWPSQYRKVFGAITTTTQFVLFFFIISIC 300

QY 247 YFKILQKVKSDMIQNAQFCQSLTQKQSDA-TSRKKKVNYYLIAMVVTFIGCWLPLTL 305

DB 301 YVWISVKLN-----QRARAKPGSKSRREADRDKKRTNRMLIAMVAVGLSWLPINNV 355

QY 306 NLVKOP-KKEPEWLKQEPFWAINAHVIAVSLVWNPPLFFWLT---RKQKRSGL----- 356

DB 356 NIFDDFDDKSNEWRFYILFFV--AHSIAWSTCTNPFYLAWLNENFRKEFKHVLPCFNP 413

QY 357 --SKILNSTEGSKKAGGSLGIGLH 380

DB 414 SNNNIINITRGYNRSDRNTC-GPRLH 438

RESULT 11

ADRO3092

ID ADRO3092 standard; protein; 600 AA.

XX

AC ADRO3092;

XX

DT 23-SEP-2004 (first entry)

XX

DE Drosophila G-protein coupled receptor DmGPCR1.

XX

KW antiasthmatic; antiarteriosclerotic; neuroprotective; antiinflammatory; gastrointestinal; atipsoriatic; antiarthritic; antirheumatic;

KW antithyroid; immunosuppressive; cardiant; cerebroprotective; vasotropic;

KW nephrotropic; cytostatic; insecticide; immune response;

KW G-protein coupled receptor; cancer; tumor growth; asthma; psoriasis;

KW inflammatory bowel disease; multiple sclerosis; thyroiditis;

KW rheumatoid arthritis; metabolic disorder; artherosclerosis;

KW autoimmune disorder; organ transplantation; myocardial infarction;

KW cardiomyopathy; stroke; renal failure;

KW oxidative stress-related neurodegenerative disorder; fruit fly; DmGPCR1;

receptor.

XX

OS Drosophila melanogaster.

XX

PN US2004121956-A1.

XX

PD 24-JUN-2004.

XX

PF 15-DEC-2003; 2003US-00736048.

XX

PR 22-OCT-1999; 99US-00425676.

PR 20-OCT-2000; 2000US-00693746.

XX

PA (LOWE/) LOWERY D E.

PA (SMIT/) SMITH V G.

PA (KUBI/) KUBIAK T M.

PA (LARS/) LARSEN M J.

XX

PI Lowery DE, Smith VG, Kubiak TM, Larsen MJ;

XX

DR WPI: 2004-468193/44.

DR N-PSDB; ADRO3091.

XX

PT Novel isolated nucleic acid molecule encoding Drosophila melanogaster G-protein coupled receptor (DmGPCR), useful in screening DmGPCR modulators for treating disorders e.g. artherosclerosis, myocardial infarction, stroke and cardiomyopathy.

XX

PS Claim 29; SEQ ID NO 2; 101pp; English.

XX

CC The invention describes a nucleic acid molecule encoding Drosophila melanogaster G-protein coupled receptor, having fully defined sequence (S1) of 1803, 1443, 1376, 1559, 1568, 1394, 1536, 1628, 1451, 1754 or 1452 nucleotides as given in specification, a sequence that encodes protein having fully defined sequence (S2) of 600, 357, 458, 519, 522, 518, 542, 483, 584 or 483 amino acids as given in specification, or a sequence complementary to (S1). Also described are: an expression vector (II) comprising (I); a host cell (III) transformed with (II); an isolated polypeptide (IV) encoded by (I); an isolated antibody (V) binding to an







SQ Sequence 376 AA;  
 Query Match 24.9%; Score 515.5; DB 4; Length 376;  
 Best Local Similarity 30.3%; Pred. No. 5.3e-45;  
 Matches 119; Conservative 78; Mismatches 131; Indels 65; Gaps 11;

QY 29 NNGSCIOAIAAAGGDDITVDYIRSIPTFLYGLFVIGFGVGLVAVARNKRLQS 88  
 DB 2 NGSDCLNLSELWLYR-EDLSRRWYIMLVFAFLYLIIAAGIIGNSCVILAITRNKSLQT 60  
 QY 89 ARNVFLNLFIPTDLILVFTALPVPYAMTKDMAFGSMCHLVPLNSCSVFVTSWLSLA 148  
 DB 61 VPNLFILSLSCSDIVVCTSATITPITAFKKEWIFGEALCRAPFIAGISLCFSTFTLTA 120  
 QY 149 ISLDKPLHNDPTKQPSVIRQALAITFLIMVSTLNLPLYMSPEHVDGSPYVQGETPY 208  
 DB 121 ISIDRYILIRPMPKPIPTHYQAVGVIAICAFATITSPIN--FKQKLGEF-----ENF 172  
 QY 209 CGHFCDEANW-QSENSRKIYGTVMLLQFVVPMAVITYCYPKILQKVSMDIIONAQFCQ 267  
 DB 173 CGQYCTE-NWGANESQRKIYGAALMFLQLVPLPIIIISYTAISLKIGQSMLKGA---- 227  
 QY 268 SLTKQKRSQ-----ATSRKKVNYILIAMVVTFTGCMWLPFLTLNLVDPFKKEP 315  
 DB 228 ---KKQKTDNWMELSDOORJAVKRRQRTNMLIGMVAFACSMWSVTFNILDYELP 284  
 QY 316 EWLKRPQPFMAINAHVIAVMSLVVNNPLLF-----FWLTRKQKRSQ--LS 357  
 DB 285 ELIKTQYVIFGIATHCIAVTSTVNNPLLYAVNLQLRAAFIDLMPHLRLHNLGDNSS 344  
 QY 358 KILN-----STGSKKAGGSLRGILQHLDP 384  
 DB 345 PLLNHTWTITNKGSKQ-----HTLIP 366

RESULT 15  
 ADN24291  
 ID ADN24291 standard; protein; 374 AA.  
 AC ADN24291,  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Bacterial polypeptide #6944.  
 XX  
 KW Recombinant DNA construct; transformed plant; improved plant property;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KW pathogen tolerance; pest tolerance; plant disease resistance;  
 KW cell cycle pathway modification; plant growth regulator;  
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 KW bacterial polypeptide.  
 XX  
 OS Bacteria.  
 XX  
 FN US2003233675-A1.  
 XX  
 PD 18-DEC-2003.  
 XX  
 PF 20-FEB-2003; 2003US-00369493.  
 XX  
 PR 21-FEB-2003; 2002US-0360039P.  
 XX  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 XX  
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
 XX WPI; 2004-061375/06.  
 DR  
 XX

PT New recombinant DNA construct comprising a promoter positioned to provide  
 PT for expression of a polynucleotide encoding a polypeptide from a  
 PT microbial source, useful for producing plants with improved properties.  
 XX  
 PS Claim 1; SEQ ID NO 6944; 122pp; English.  
 XX  
 CC The invention relates to a recombinant DNA construct comprising a  
 CC promoter functional in a plant cell, where the promoter is positioned to  
 CC provide for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source. The invention also relates to a transformed plant  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC having an improved property comprises transforming a plant with the  
 CC recombinant DNA construct and growing the transformed plant, where the  
 CC polynucleotide or polypeptide is useful for improving plant properties.  
 CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition, improved lignin production or improved galactomannan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.  
 XX  
 SQ Sequence 374 AA;  
 Query Match 24.8%; Score 514; DB 8; Length 374;  
 Best Local Similarity 31.3%; Pred. No. 7.6e-45;  
 Matches 114; Conservative 74; Mismatches 128; Indels 48; Gaps 9;

QY 29 NNGSCIOAIAAAGGDDITVDYIRSIPTFLYGLFVIGFGVGLVAVARNKRLQS 88  
 DB 2 NGSDCLNLSELWLYR-EDLSRRWYIMLVFAFLYLIIAAGIIGNSCVILAITRNKSLQT 60  
 QY 89 ARNVFLNLFIPTDLILVFTALPVPYAMTKDMAFGSMCHLVPLNSCSVFVTSWLSLA 148  
 DB 61 VPNLFILSLSCSDIVVCTSATITPITAFKKEWIFGEALCRAPFIAGISLCFSTFTLTA 120  
 QY 149 ISLDKPLHNDPTKQPSVIRQALAITFLIMVSTLNLPLYMSPEHVDGSPYVQGETPY 208  
 DB 121 ISIDRYILIRPMPKPIPTHYQAVGVIAICAFATITSPIN--FKQKLGEF-----ENF 172  
 QY 209 CGHFCDEANW-QSENSRKIYGTVMLLQFVVPMAVITYCYPKILQKVSMDIIONAQFCQ 267  
 DB 173 CGQYCTE-NWGANESQRKIYGAALMFLQLVPLPIIIISYTAISLKIGQSMLKGA---- 227  
 QY 268 SLTKQKRSQ-----ATSRKKVNYILIAMVVTFTGCMWLPFLTLNLVDPFKKEP 315  
 DB 228 ---KKQKTDNWMELSDOORJAVKRRQRTNMLIGMVAFACSMWSVTFNILDYELP 284  
 QY 316 EWLKRPQPFMAINAHVIAVMSLVVNNPLLF-----FWLTRKQKRSQ--LS 357  
 DB 285 ELIKTQYVIFGIATHCIAVTSTVNNPLLYAVNLQLRAAFIDLMPHLRLHNLGDNSS 344  
 QY 358 KILN-----ATSRKKVNYILIAMVVTFTGCMWLPFLTLNLVDPFKKEP 315  
 DB 345 PLLNHTWTITNKGSKQ-----HTLIP 366

Search completed: May 8, 2006, 09:29:35  
 Job time: 191 secs



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OM protein - protein search, using sw model

Run on: May 8, 2006, 09:34:27 ; Search time 166 Seconds  
(without alignments)  
999.267 Million cell updates/sec

Title: US-10-650-467-105  
Perfect score: 2074  
Sequence: 1 MVSSAATISTITTTPTPI.....QLHLLPTSTHSDRCAGNSF 397

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
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6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2074	100.0	397	5	US-10-650-467-105
2	2074	100.0	499	5	US-10-650-467-40
3	1899	91.6	433	5	US-10-650-467-107
4	607.5	29.3	450	5	US-10-650-467-16
5	607.5	29.3	539	4	US-10-369-493-6608
6	529	25.5	518	3	US-09-804-5518-8
7	529	25.5	600	4	US-10-283-423-2
8	529	25.5	600	4	US-10-213-821-2
9	529	25.5	600	4	US-10-736-048-2
10	529	25.5	600	5	US-10-489-423-62
11	529	25.5	600	6	US-11-097-143-41472
12	515.5	24.9	376	5	US-10-650-467-22
13	514	24.8	374	4	US-10-369-493-6944
14	485.5	23.4	457	4	US-10-369-493-6769
15	485.5	23.4	457	5	US-10-650-467-26
16	461.5	22.3	365	4	US-10-369-493-6958
17	461.5	22.3	365	5	US-10-650-467-36
18	460.5	22.2	387	5	US-10-650-467-14
19	458	22.1	381	5	US-10-650-467-12
20	458	22.1	402	5	US-10-650-467-8
21	458	22.1	404	5	US-10-650-467-6
22	458	22.1	406	5	US-10-650-467-10
23	419.5	20.2	412	4	US-10-369-493-6883
24	390.5	18.8	375	4	US-10-081-810-51
25	388	18.7	458	4	US-10-283-423-6
26	388	18.7	458	4	US-10-213-821-6
27	388	18.7	458	4	US-10-736-048-6

ALIGNMENTS

RESULT 1

US-10-650-467-105

; Sequence 105, Application US/10650467

; Publication No. US20050176069A1

; GENERAL INFORMATION:

; APPLICANT: Lowery, David E.

; APPLICANT: Geary, Timothy G.

; APPLICANT: Kubiak, Teresa M.

; APPLICANT: Larsen, Martha J.

; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS

; FILE REFERENCE: 28341/6223

; CURRENT APPLICATION NUMBER: US/10/650,467

; CURRENT FILING DATE: 2003-08-28

; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870

; PRIOR FILING DATE: CURRENT FILING DATE: 2000-11-24

; NUMBER OF SEQ ID NOS: 180

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 105

; LENGTH: 397

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-650-467-105

Query Match	100.0%	Score 2074;	DB 5;	Length 397;
Best Local Similarity	100.0%	Pred. No. 1.9e-174;	Mismatches 0;	Indels 0;
Matches 397;	Conservative 0;			Gaps 0;
Qy	1	MVSSAATISTITTTPTPI	SHSNNGSCIQAIAAAGQIDDDITVDYFIRSIPTF	60
Db	1	MVSSAATISTITTTPTPI	SHSNNGSCIQAIAAAGQIDDDITVDYFIRSIPTF	60
Qy	61	LYGFLVVGIFGNGVLWAVARNKELQARNVFLNLFTDLILVFTAIPTVPTWAMTKD	120	
Db	61	LYGFLVVGIFGNGVLWAVARNKELQARNVFLNLFTDLILVFTAIPTVPTWAMTKD	120	
Qy	121	WAFGVMCHLVPLNSCSVFVTSWLSLTALSLDKFHINDPTKQPVSIROALAITFLIWLIV	180	
Db	121	WAFGVMCHLVPLNSCSVFVTSWLSLTALSLDKFHINDPTKQPVSIROALAITFLIWLIV	180	
Qy	181	STLINLPYLMGFEHVDGSGFYVQPGTPTCYCGHFCDEANQSENRSKIYGTVMVLLQFVWPM	240	
Db	181	STLINLPYLMGFEHVDGSGFYVQPGTPTCYCGHFCDEANQSENRSKIYGTVMVLLQFVWPM	240	
Qy	241	AVITYCYFKILQKVKSMIIQNAQPCQSLTKQSDATSRKKKNYILIAMVVTFIGWL	300	
Db	241	AVITYCYFKILQKVKSMIIQNAQPCQSLTKQSDATSRKKKNYILIAMVVTFIGWL	300	
Qy	301	PLTLINLVKDFKKEPEWLKROPFFWAINAHVIAVMSLVVWNPILLFWLTKRKGSGLSKIL	360	
Db	301	PLTLINLVKDFKKEPEWLKROPFFWAINAHVIAVMSLVVWNPILLFWLTKRKGSGLSKIL	360	

Qy 361 NSTEGSKAGSGLRGIQLHDLPTSTHSDRCAGNSF 397  
|||

Db 361 NSTEGSKAGSGLRGIQLHDLPTSTHSDRCAGNSF 397  
|||

RESULT 2  
US-10-650-467-40  
; Sequence 40, Application US/10650467  
; Publication No. US20050176069A1

; APPLICANT: LOWERY, David E.  
 ; APPLICANT: Geary, Timothy G.  
 ; APPLICANT: Kubiak, Teresa M.  
 ; APPLICANT: Larsen, Martha J.

```

; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/10/650,467
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER

```

```

; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 400

```

US-10-650-467-40

	Matches	397;	Conservative	0;	Mismatches	0;
Qy	1	MYSSAATISTTSTTTTPSTTSNVITSHSNGSGCTQIAEAIAIA				

QY 61 LYGFLFVLGIFGNGGVLWAVARNKQLQARNVFLNLIFTD

[illegible]

Db 283 STILNLPYLMSPFHVDSFYVQGPETPYCGHFCDEANWQSE

343 AVITYCYFKILQVSKDMIIQNAQPCQSLTKQKQSDATSRKK  
301 PVTLLNLVQPKCKEPEWLKQOPFFFWAINAHVIAWSLVVWNP

DD	403	PZILLENVVKDFNCEPFWLAKQFFFWAINCHVILAGSLVVRN
QY	361	NSTEGSKAGGSLRGIQLHLLPTSTHSDRCAGNSF 3977

RESULT 3  
US-10-650-467-107

; PUBLICATION NO. US20050176069A1  
 ;  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Lowery, David E.  
 ;  
 ; APPLICANT: Geary, Timothy G.

; APPLICANT: Larsen, Martha J.  
 ; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED  
 ; FILE REFERENCE: 28341/8223

Db 9 CIDVNAIL--QQFNDWTVLFEVLGYSVLYFLIILIGLVGNGLLITSIILMRKCL-SVANI 65  
QY 93 FLNLIFLTDLILVFTAIPTVTPWYAMTKOWAFGSMCHLVPLNSCSVFVTSWLSLTAISLD 152  
Db 66 FLINLAVSDDLCCITAVPTIPVLAFMKRWIFGIIMCKLVPTCOAFSVLSSSLCYAID 125  
QY 153 KEFLHNDPTKQPVSIHQALAITFLIIVSTLINLPYLMSEFHVDSFVYQPGET----- 206  
Db 126 RYRSIVTPLREPSDRHARWLLMFTWVAFSLAYPL-----YYSQNLKTMVIENV 175  
QY 207 PYCGHFCDANWQSENSRKI-YGTTVMLLQFVVPMAVITYCYFKILQKVKSKDMLIQNAQF 265  
Db 176 TLCDGFCGFNFQSDSEISKLYTTSLLIIQLIIPAIMSFCYLMILQKVQTDWLVDGSM 235  
QY 266 CQSLTKQKSDATSRKKKNYILIAMVVTFIGCWLPLTLNLVKDFKCKPEW----- 317  
Db 236 ---LTAQAQATAVRKRVRMYVILMVIVFMAWFLSAVNLFRDLGMRPEFCQTVYKVL 292  
QY 318 LKQRPFFWAINAHVIAVSLVWNPPLLFWLTRKQKRS 354  
Db 293 MMDQMTFKLLNVHVIAMTSIVMNPVLYFWMSKRRRA 329

## RESULT 5

US-10-369-493-6608  
; Sequence 6608, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; PRIOR FILING DATE: 2003-02-28  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 6608  
; LENGTH: 539  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-10-369-493-6608

Query Match 29.3%; Score 607.5; DB 4; Length 539;  
Best Local Similarity 35.3%; Pred. No. 7.8e-45;  
Matches 119; Conservative 76; Mismatches 111; Indels 31; Gaps 7;  
QY 33 CIOIAEAIQAAGDIDTVDFYRSIFTLGYFLVIGFNGGVLWAVARNKRLQARNV 92  
Db 9 CIDVNAIL--QQFNDWTVLFEVLGYSVLYFLIILIGLVGNGLLITSIILMRKCL-SVANI 65  
QY 93 FLNLIFLTDLILVFTAIPTVTPWYAMTKOWAFGSMCHLVPLNSCSVFVTSWLSLTAISLD 152  
Db 66 FLINLAVSDDLCCITAVPTIPVLAFMKRWIFGIIMCKLVPTCOAFSVLSSSLCYAID 125  
QY 153 KEFLHNDPTKQPVSIHQALAITFLIIVSTLINLPYLMSEFHVDSFVYQPGET----- 206  
Db 126 RYRSIVTPLREPSDRHARWLLMFTWVAFSLAYPL-----YYSQNLKTMVIENV 175  
QY 207 PYCGHFCDANWQSENSRKI-YGTTVMLLQFVVPMAVITYCYFKILQKVKSKDMLIQNAQF 265  
Db 176 TLCDGFCGFNFQSDSEISKLYTTSLLIIQLIIPAIMSFCYLMILQKVQTDWLVDGSM 235  
QY 266 CQSLTKQKSDATSRKKKNYILIAMVVTFIGCWLPLTLNLVKDFKCKPEW----- 317  
Db 236 ---LTAQAQATAVRKRVRMYVILMVIVFMAWFLSAVNLFRDLGMRPEFCQTVYKVL 292  
QY 318 LKQRPFFWAINAHVIAVSLVWNPPLLFWLTRKQKRS 354

Db 293 MMDQMTFKLLNVHVIAMTSIVMNPVLYFWMSKRRRA 329  
RESULT 6  
US-09-804-551B-8  
; Sequence 8, Application US/09804551B  
; Patent No. US20020056151A1  
; GENERAL INFORMATION:  
; APPLICANT: Bayer Aktiengesellschaft  
; TITLE OF INVENTION: Receptors for peptides from insects  
; FILE REFERENCE: Le A 34 394  
; CURRENT APPLICATION NUMBER: US/09/804,551B  
; CURRENT FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: DE 100 13 618.4  
; PRIOR FILING DATE: 2000-03-18  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 518  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-804-551B-8  
Query Match 25.5%; Score 529; DB 3; Length 518;  
Best Local Similarity 30.5%; Pred. No. 6.4e-38;  
Matches 136; Conservative 154; Mismatches 158; Indels 80; Gaps 12;  
QY 6 ATISTISTTTTPTST-----ISNVITSHSNNGSCIOIAEAIQAAGID---DITVDFY 53  
Db 2 ANLSWLSITTTTSSSISTSQLPLVSTTNWLSLPGTTSAILADVAASDEDRSGIHNQF 61  
QY 54 IRSIFTFYGLFVLGIFGNGVLMVAVARNKRLQSAARNVPLMLIFTDLILVFTAIPTVTP 113  
Db 62 VOIFPFVLYATVFLGVFGNVLVCYVVLNRAMQTVTNIFITNLALSDILLCLVALVPFP 121  
QY 114 WTAMTKOWAFGSMCHLVPLNSCSVFVTSWLSLTAISDKFLHNDPTKQPVSIHQALAI 173  
Db 122 LYTFMGRWAFGRSLCHLVSAQGCISIYSTLTSLTSLTSLTSLTSLTSLTSLTSLTSLT 181  
QY 174 TFLIIVSTLINLPYLMSEF-----HVDGGSFYVQPG----- 204  
Db 182 IVSIWIALLATVPGMYMKMTNELVNGTQNETLVEATLMLNGSFVAQGSFIFAPDS 241  
QY 205 -----ETPYCGHFCDANWQSENSRKIYGTVMLLQFVVPMAVITYC 246  
Db 242 TSATQAYMQVMTAGSTGPEMPYRVYCEB-NWPEQYRKVFGAITTTTLQFVLPPFIISIC 300  
QY 247 YFKILQKVKSKDMLIQNAQFCQSLTKQKSDA-TSRKKKNYILIAMVVTFIGCWLPLTLL 305  
Db 301 YWVISVKLN-----QRARAKPGSKSRREADRDRKRTNRMLIAMVAVFGLSWLPINVV 355  
QY 306 NLVKDFP-KKEPEWLKRPFPFMAINAHVIAVSLVWNPPLLFWLT---RKQKRSGL----- 356  
Db 356 NIFDDFDKSNRWFVILEFFV--AHSIAWSTCTNPFLLYMLNENFRKFKHVLPCFNP 413  
QY 357 --SKILNSTEGSKAGGSLGRLQLH 380  
Db 414 SNNNIINITRGYNRSDRNTC-GPRLH 438

## RESULT 7

US-10-283-423-2  
; Sequence 2, Application US/10283423  
; Publication No. US20030162223A1  
; GENERAL INFORMATION:  
; APPLICANT: Lowery, David E.  
; APPLICANT: Smith, Valdin G.  
; APPLICANT: Kubiak, Teresa M.  
; APPLICANT: Larsen, Martha J.  
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Metho  
; FILE REFERENCE: PHR00002-102

```
; Application Project
;
; CURRENT APPLICATION NUMBER: US/10/283,423
; CURRENT FILING DATE: 2002-10-30
; Earlier Applications
;
; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/693,746
; PRIOR FILING DATE: PriorFilingDate : 2000-10-20
; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/425,676
; PRIOR FILING DATE: PriorFilingDate : 1999-10-22
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 600
; TYPE: PRT
; ORGANISM: D. melanogaster
US-10-283-423-2

Query Match      25.5%; Score 529; DB 4; Length 600;
Best Local Similarity 30.5%; Pred. No. 7.6e-38;
Matches 136; Conservative 76; Mismatches 154; Indels 80; Gaps 12;

QY 6 ATISTITTTTPTST-----ISNVITSHNNNGSCIQIAEATAAQGID---DITVDYF 53
Db 2 ANLSWLSTITTTSSISSTSQLPLVSTTNWLSLTPGTTSAILLADVAASDEDRSGGIHNQF 61

QY 54 IRSITFTLYGLFVLGIFGNGGVLMVARNKRLQSAARNVFLNLIFTDLILVFTAIPVTP 113
Db 62 VOIPFYVLYATVFLVGVGNVLCVVLNRRAMQTVTNFITNLALSILLCVLAVPFTP 121

QY 114 WYAMTKWAFGVMCHLVPLNSCSVFVTSWLSLTAISLDKFLHINDPTKQPVSIQALAI 173
Db 122 LYTFMGRWAFGRSLCHLVSPAQGCISYISTLTLSIAIDRYFVLIYPHPRMKLSCTGIG 181

QY 174 TPLIWIIVSTLINLPYMSFE-----HVDGSFYVQPG----- 204
Db 182 IVSIWVIALLATVPYGMVMTNMLVNGTQGTNETLVEATLMLNGSFVAQSGPTEAPDS 241

QY 205 -----ETPCYGHFCDEANWQSENRSKIYTTVMLLQFVVPMAVIYTC 246
Db 242 TSATQAYMQVMTAGTGPMPYRVYCEE-NWPSEQYRKVFGAITTTLQFVLPFFIISIC 300

QY 247 YPKILQKYSKMIQNAQPCQSLTKQRSDA-TSRKKKNVYLLIAMVTFICWMLPLTLL 305
Db 301 YVMISVKLN-----QRARAKPGSKSRREEDRDKRTNRMLIAMVAVFGLSWLPINVV 355

QY 306 NLVKDPF-KCEPEWLKRPFFWAINAHVIAVMSLVVNNPLLPFWLT---RKQKRSGL----- 356
Db 356 NIPDFDDKSNWRFYILFFV--AHSIAMSTCYNPFYAWLNENFRKPKHVLPCFNP 413

QY 357 ---SKILNSTEGSKKAGGSLRGILQH 380
Db 414 SNNNIINITRGYNRSRNTC-GPRLH 438

RESULT 8
US-10-213-821-2
; Sequence 2, Application US/10213821
; Publication No. US20030180297A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; TITLE OF INVENTION: Related To The Same
; FILE REFERENCE: 6297,2CD
; CURRENT APPLICATION NUMBER: US/10/213,821
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 09/693,746
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/425,676
```

```
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 600
; TYPE: PRT
; ORGANISM: D. melanogaster
US-10-213-821-2

Query Match      25.5%; Score 529; DB 4; Length 600;
Best Local Similarity 30.5%; Pred. No. 7.6e-38;
Matches 136; Conservative 76; Mismatches 154; Indels 80; Gaps 12;

QY 6 ATISTITTTTPTST-----ISNVITSHNNNGSCIQIAEATAAQGID---DITVDYF 53
Db 2 ANLSWLSTITTTSSISSTSQLPLVSTTNWLSLTPGTTSAILLADVAASDEDRSGGIHNQF 61

QY 54 IRSITFTLYGLFVLGIFGNGGVLMVARNKRLQSAARNVFLNLIFTDLILVFTAIPVTP 113
Db 62 VOIPFYVLYATVFLVGVGNVLCVVLNRRAMQTVTNFITNLALSILLCVLAVPFTP 121

QY 114 WYAMTKWAFGVMCHLVPLNSCSVFVTSWLSLTAISLDKFLHINDPTKQPVSIQALAI 173
Db 122 LYTFMGRWAFGRSLCHLVSPAQGCISYISTLTLSIAIDRYFVLIYPHPRMKLSCTGIG 181

QY 174 TPLIWIIVSTLINLPYMSFE-----HVDGSFYVQPG----- 204
Db 182 IVSIWVIALLATVPYGMVMTNMLVNGTQGTNETLVEATLMLNGSFVAQSGPTEAPDS 241

QY 205 -----ETPCYGHFCDEANWQSENRSKIYTTVMLLQFVVPMAVIYTC 246
Db 242 TSATQAYMQVMTAGTGPMPYRVYCEE-NWPSEQYRKVFGAITTTLQFVLPFFIISIC 300

QY 247 YPKILQKYSKMIQNAQPCQSLTKQRSDA-TSRKKKNVYLLIAMVTFICWMLPLTLL 305
Db 301 YVMISVKLN-----QRARAKPGSKSRREEDRDKRTNRMLIAMVAVFGLSWLPINVV 355

QY 306 NLVKDPF-KCEPEWLKRPFFWAINAHVIAVMSLVVNNPLLPFWLT---RKQKRSGL----- 356
Db 356 NIPDFDDKSNWRFYILFFV--AHSIAMSTCYNPFYAWLNENFRKPKHVLPCFNP 413

QY 357 ---SKILNSTEGSKKAGGSLRGILQH 380
Db 414 SNNNIINITRGYNRSRNTC-GPRLH 438

RESULT 9
US-10-736-048-2
; Sequence 2, Application US/10736048
; Publication No. US20040121956A1
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; TITLE OF INVENTION: Related To The Same
; FILE REFERENCE: 6297,1cp
; CURRENT APPLICATION NUMBER: US/10/736,048
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US/09/693,746
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/425,676
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 600
; TYPE: PRT
; ORGANISM: D. melanogaster
US-10-736-048-2

Query Match      25.5%; Score 529; DB 4; Length 600;
```

Best Local Similarity 30.5%; Pred. No. 7.6e-38;  
Matches 136; Conservative 76; Mismatches 154; Indels 80; Gaps 12;

```
QY 6 ATISTITTTTPT-----ISNVITSHNNGSCIOIAEIAAAGID---DITVDYF 53
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILDVAASDEDRSGGIHQF 61
QY 54 IRSIFFLYGLFVLGIFGNGVGLWAVARNKRLQSAARNVFLNLIPTDLILVFTAIPTVP 113
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 VQIFFVLVATVFLGVFGVNLVCYVVLNRAMQVTNIPITLALSDILLCLVLAFFPTP 121
QY 114 WYAMTKDWAFGSMCHLVPLNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIROALAI 173
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
122 LYTFMGRWAFGRSLCHLVSPAQCSYIYSTLTLSIAIDRYFVLIYFFPHPRMKLSTCIGI 181
QY 174 TFLIWIVSTLINLPYLMSE-----HVDGSFYVQPG----- 204
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
182 IVSIWIALLATVPYGYMKMTNELVNGTGTNETILVEATMLNGSFVAQGSFIEAPDS 241
QY 205 -----ETPYCGHFCDEANWSENRSKIYGTVMLLQFVVPMAVITVC 246
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
242 TSATQAYMQVMTAGSTGPEMPYRVVYCEB--NWPSEQYRKVFGAITTTLOFVLPPFIISIC 300
QY 247 YFKILQKSKDMIQNAQFCQSLTKQSDA--TSRKKKNYILIAMVVTFIGCWLPLTLL 305
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
301 YWISVKLN-----QARAKPGSKSRREADRDRKRTNRMLIANVAVFGLSWLPINVV 355
QY 306 NLVKDF--KKEPEWLKRPFFMAINAHVIAVMSLVVWNPPLFFWLT---RKQKRSGL----- 356
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
356 NIPDDPDDKSNEWRFYILFFV--AHSIAMSTCYNPFYLAWLNFNFRKFKHVLPCFNP 413
QY 357 --SKILNSTEGSKKAGGSLRGILQH 380
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
414 SNNNIINITRGYNRSRNTC-GPRLH 438
```

## RESULT 10

```
US-10-489-425-62
; Sequence 62, Application US/10489425
; Publication No. US20040248791A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations AG
; APPLICANT: Spana, Eric
; APPLICANT: Kamdar, Kim
; APPLICANT: Stam, Lynn
; APPLICANT: Valentine, Scott
; APPLICANT: Griswald, Charles M
; TITLE OF INVENTION: Insect G Protein-Coupled Receptor Genes and Uses thereof
; FILE REFERENCE: 60134WOPCT
; CURRENT APPLICATION NUMBER: US/10/489,425
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: 60/341,512
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 62
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-489-425-62
```

Query Match 25.5%; Score 529; DB 5; Length 600;  
Best Local Similarity 30.5%; Pred. No. 7.6e-38;  
Matches 136; Conservative 76; Mismatches 154; Indels 80; Gaps 12;

```
QY 6 ATISTITTTTPT-----ISNVITSHNNGSCIOIAEIAAAGID---DITVDYF 53
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILDVAASDEDRSGGIHQF 61
QY 54 IRSIFFLYGLFVLGIFGNGVGLWAVARNKRLQSAARNVFLNLIPTDLILVFTAIPTVP 113
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 VQIFFVLVATVFLGVFGVNLVCYVVLNRAMQVTNIPITLALSDILLCLVLAFFPTP 121
```

```
QY 114 WYAMTKDWAFGSMCHLVPLNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIROALAI 173
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
122 LYTFMGRWAFGRSLCHLVSPAQCSYIYSTLTLSIAIDRYFVLIYFFPHPRMKLSTCIGI 181
QY 174 TFLIWIVSTLINLPYLMSE-----HVDGSFYVQPG----- 204
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
182 IVSIWIALLATVPYGYMKMTNELVNGTGTNETILVEATMLNGSFVAQGSFIEAPDS 241
QY 205 -----ETPYCGHFCDEANWSENRSKIYGTVMLLQFVVPMAVITVC 246
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
242 TSATQAYMQVMTAGSTGPEMPYRVVYCEB--NWPSEQYRKVFGAITTTLOFVLPPFIISIC 300
QY 247 YFKILQKSKDMIQNAQFCQSLTKQSDA--TSRKKKNYILIAMVVTFIGCWLPLTLL 305
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
301 YWISVKLN-----QARAKPGSKSRREADRDRKRTNRMLIANVAVFGLSWLPINVV 355
QY 306 NLVKDF--KKEPEWLKRPFFMAINAHVIAVMSLVVWNPPLFFWLT---RKQKRSGL----- 356
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
356 NIPDDPDDKSNEWRFYILFFV--AHSIAMSTCYNPFYLAWLNFNFRKFKHVLPCFNP 413
QY 357 --SKILNSTEGSKKAGGSLRGILQH 380
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
414 SNNNIINITRGYNRSRNTC-GPRLH 438
```

## RESULT 11

```
US-11-097-143-41472
; Sequence 41472, Application US/11097143
; Publication No. US2005020858A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41472
; LENGTH: 600
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-41472
```

Query Match 25.5%; Score 529; DB 6; Length 600;  
Best Local Similarity 30.5%; Pred. No. 7.6e-38;  
Matches 136; Conservative 76; Mismatches 154; Indels 80; Gaps 12;

```
QY 6 ATISTITTTTPT-----ISNVITSHNNGSCIOIAEIAAAGID---DITVDYF 53
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILDVAASDEDRSGGIHQF 61
QY 54 IRSIFFLYGLFVLGIFGNGVGLWAVARNKRLQSAARNVFLNLIPTDLILVFTAIPTVP 113
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 VQIFFVLVATVFLGVFGVNLVCYVVLNRAMQVTNIPITLALSDILLCLVLAFFPTP 121
```

114 WYAMTKDWAQFSGVMCHLVPNSCSVFTVTSLSLTALDKLPHINDPTKQPVSRQALAI 173  
122 LYTFMGRWAFGRSLCHLVSPAQCCSIYISTLTLSIAIDRVPIIYPPHPRMKLSTCIGI 181  
174 TFLIIVSTLNLPLYLMSFGE-----HVDGPFVQPG----- 204  
182 IVSIVWIALLATVPVGMVOMTNELVNGTQGTNEVLATMLNGSFVAQSGGFIEAPDS 241  
205 -----ETPYCGHFCDEANWQSENRSKIYGTVMQLQFVVPMVAIYTC 246  
242 TSATQAVQVMTAGTGPMPYRVYCEB-NWPSQYKRVFCATITTLQFVLPFFIISIC 300  
247 YPKILQKVKMDIQAQFCQSLTQKQSDA-TSRKKKNYILIAMVTFICWMLPLTL 305  
285 ELIKTQYIFGIATHCIAMTSTVWNPPLYAVLNQLRAAFIDLMPHLRHLNLEGDNSS 344  
301 YVWISVGLN-----QRAKAPGSKSRREBDRDRKTRNMLIAMVAVFGLSWLPINVV 355  
306 NLVADP-KKEPEWLRQPPFMAINAHVIAVMSLVVWNPPLLFFWLT---RKQKRSGL----- 356  
356 NIFDDPDKSKNEWRPIILFFV--AHSIAMSSTCYNPFLYAWLNENPRKEPKHVLPCFNP 413  
357 --SKLNSTEGSKKAGGSLRGIQLH 380  
414 SNNNIINITRGVNRSDRNTC-GPRLH 438

## RESULT 12

US-10-650-467-22  
; Sequence 22, Application US/10650467  
; Publication No. US20050176069A1  
; GENERAL INFORMATION:  
; APPLICANT: Lowery, David B.  
; APPLICANT: Geary, Timothy G.  
; APPLICANT: Kubiak, Teresa M.  
; APPLICANT: Larsen, Martha J.  
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 28341/6223  
; CURRENT APPLICATION NUMBER: US/10/650,467  
; CURRENT FILING DATE: 2003-08-28  
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870  
; PRIOR FILING DATE: CURRENT FILING DATE: 2000-11-24  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 376  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-650-467-22

Query Match 24.9%; Score 515.5; DB 5; Length 376;  
Best Local Similarity 30.3%; Pred. No. 6.7e-37;  
Matches 119; Conservative 78; Mismatches 131; Indels 65; Gaps 11;

QY 29 NNGSCIOIAEAAAGGIDITVDVFIKRSIFLYGFLVGLFGNGGVLMAVARNKRLQS 88  
DB 2 NGSDCLNLSLWLYR-EDLSRWYIMLVFAFLYLIITAAAGLIGNSCVILATRNKSLQT 60  
QY 89 ARNVFLNLIFTLILVFTAPVTPWYAMTKDWAQFSGVMCHLVPNSCSVFTVTSLSLT 148  
DB 61 VPNLFILSLSCSDIVVCCTSATITPITAPKKEWIFGEALCRAPFIAGISLCFSFTLTA 120  
QY 149 ISLDFPLHNDPTKQPVSIROALATFLIWIIVSTLINPLYMSFHVDSFVQGPETPY 208  
DB 121 ISIDRYILIRFPMRKPITHYQAVGVIAICAFATITSPIM--FKQKLGEP-----ENF 172  
QY 209 CGHFCDEANW-QSENRSKIYGTVMQLQFVPMVAIYTCYFKILQKVKMDIQAQFCQ 267  
DB 173 CQCYCTE-NWGANESQRIYGAALMFLQLVPLTIIISYTAISLKIGQSMILKGA---- 227  
QY 268 SITQKQKQSD-----ATSRKKKNYILIAMVTFICWMLPLTLNLVADKPFKEP 315  
DB 228 ---KKQKTDNWEMLSDQORIAVGRQRTNRMLGNVAVAFACSWIWSVTFNLRDEYILP 284  
QY 316 BMLKQPPFMAINAHVIAVMSLVVWNPPLLFF-----FWLTRKQKRSGL--LS 357  
DB 285 ELIKTQYIFGIATHCIAMTSTVWNPPLYAVLNQLRAAFIDLMPHLRHLNLEGDNSS 344  
QY 358 KILN 361  
DB 345 PLLN 348

## RESULT 14

US-10-369-493-6769  
; Sequence 6769, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.

QY 316 BMLKQPPFMAINAHVIAVMSLVVWNPPLLFF-----FWLTRKQKRSGL--LS 357  
DB 285 ELIKTQYIFGIATHCIAMTSTVWNPPLYAVLNQLRAAFIDLMPHLRHLNLEGDNSS 344  
QY 358 KILN-----STEGSKKAGGSLRGIQLHDLIP 384  
DB 345 PLLNHTWTITNKPSKQ-----HTLIP 366

## RESULT 13

US-10-369-493-6944  
; Sequence 6944, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 6944  
; LENGTH: 374  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-10-369-493-6944

Query Match 24.8%; Score 514; DB 4; Length 374;  
Best Local Similarity 31.3%; Pred. No. 9.1e-37;  
Matches 114; Conservative 74; Mismatches 128; Indels 48; Gaps 9;

QY 29 NNGSCIOIAEAAAGGIDITVDVFIKRSIFLYGFLVGLFGNGGVLMAVARNKRLQS 88  
DB 2 NGSDCLNLSLWLYR-EDLSRWYIMLVFAFLYLIITAAAGLIGNSCVILATRNKSLQT 60  
QY 89 ARNVFLNLIFTLILVFTAPVTPWYAMTKDWAQFSGVMCHLVPNSCSVFTVTSLSLT 148  
DB 61 VPNLFILSLSCSDIVVCCTSATITPITAPKKEWIFGEALCRAPFIAGISLCFSFTLTA 120  
QY 149 ISLDFPLHNDPTKQPVSIROALATFLIWIIVSTLINPLYMSFHVDSFVQGPETPY 208  
DB 121 ISIDRYILIRFPMRKPITHYQAVGVIAICAFATITSPIM--FKQKLGEP-----ENF 172  
QY 209 CGHFCDEANW-QSENRSKIYGTVMQLQFVPMVAIYTCYFKILQKVKMDIQAQFCQ 267  
DB 173 CQCYCTE-NWGANESQRIYGAALMFLQLVPLTIIISYTAISLKIGQSMILKGA---- 227  
QY 268 SITQKQKQSD-----ATSRKKKNYILIAMVTFICWMLPLTLNLVADKPFKEP 315  
DB 228 ---KKQKTDNWEMLSDQORIAVGRQRTNRMLGNVAVAFACSWIWSVTFNLRDEYILP 284  
QY 316 BMLKQPPFMAINAHVIAVMSLVVWNPPLLFF-----FWLTRKQKRSGL--LS 357  
DB 285 ELIKTQYIFGIATHCIAMTSTVWNPPLYAVLNQLRAAFIDLMPHLRHLNLEGDNSS 344  
QY 358 KILN 361  
DB 345 PLLN 348





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OM protein - protein search, using sw model

Run on: May 8, 2006, 09:35:22 ; Search time 28 Seconds  
(without alignments)  
656.251 Million cell updates/sec

Title: US-10-650-467-105  
Perfect score: 2074  
Sequence: 1 MVSSAATISITSTTPSTI.....QLHDLPTSTHRCAGNSF 397

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:  
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2: /SIDSS5/ptodata/2/pubpaa/US06\_NEW\_PUB.pep1:  
3: /SIDSS5/ptodata/2/pubpaa/US07\_NEW\_PUB.pep1:  
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7: /SIDSS5/ptodata/2/pubpaa/US09\_NEW\_PUB.pep1:  
8: /SIDSS5/ptodata/2/pubpaa/US10\_NEW\_PUB.pep1:  
9: /SIDSS5/ptodata/2/pubpaa/US11\_NEW\_PUB.pep1:  
10: /SIDSS5/ptodata/2/pubpaa/US11\_NEW\_PUB.pep1:  
11: /SIDSS5/ptodata/2/pubpaa/US11\_NEW\_PUB.pep1:  
12: /SIDSS5/ptodata/2/pubpaa/US60\_NEW\_PUB.pep1:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	348.5	16.8	384	9 US-10-987-856-15	Sequence 15, Appl
2	346.5	16.7	384	11 US-11-080-991-26	Sequence 26, Appl
3	346.5	16.7	384	11 US-11-183-615-4	Sequence 4, Appl
4	324	15.6	381	9 US-10-987-856-16	Sequence 16, Appl
5	314	15.1	375	9 US-10-987-856-17	Sequence 17, Appl
6	304	14.7	420	9 US-10-992-577-6	Sequence 6, Appl
7	304	14.7	522	9 US-10-510-018-2	Sequence 2, Appl
8	286.5	13.8	254	9 US-10-055-877-248	Sequence 248, App
9	286.5	13.8	254	9 US-10-055-877-327	Sequence 327, App
10	286.5	13.8	254	9 US-10-055-877-340	Sequence 340, App
11	286.5	13.8	254	9 US-10-877-346-83	Sequence 83, Appl
12	285.5	13.8	430	9 US-10-992-577-8	Sequence 8, Appl
13	285.5	13.8	430	9 US-10-508-892-2	Sequence 2, Appl
14	285.5	13.8	430	11 US-11-223-294-54	Sequence 54, Appl
15	285.5	13.8	432	9 US-10-992-577-2	Sequence 2, Appl
16	285.5	13.8	432	11 US-11-223-294-37	Sequence 37, Appl
17	284	13.7	417	9 US-10-992-577-44	Sequence 44, Appl
18	274.5	13.2	394	11 US-11-183-615-17	Sequence 17, Appl
19	274.5	13.2	388	9 US-10-995-561-838	Sequence 838, App
20	274.5	13.2	389	9 US-10-995-561-837	Sequence 837, App
21	271.5	13.1	393	10 US-11-304-129-40	Sequence 40, Appl

22	267	12.9	383	9 US-10-504-588-8	Sequence 8, Appl
23	267	12.9	383	10 US-11-304-129-48	Sequence 48, Appl
24	266.5	12.8	400	11 US-11-127-877-55	Sequence 55, Appl
25	262.5	12.7	259	9 US-10-055-877-225	Sequence 225, App
26	262.5	12.7	259	9 US-10-055-877-237	Sequence 237, App
27	262.5	12.7	259	11 US-11-206-587-27	Sequence 27, Appl
28	262.5	12.7	259	11 US-11-206-587-29	Sequence 29, Appl
29	261.5	12.6	359	8 US-10-511-937-2990	Sequence 49, Appl
30	261	12.6	381	10 US-11-304-129-49	Sequence 2990, App
31	261	12.6	384	9 US-10-504-588-2	Sequence 2, Appl
32	261	12.6	384	10 US-11-304-129-36	Sequence 36, Appl
33	261	12.6	384	11 US-11-073-420-7	Sequence 7, Appl
34	260.5	12.6	380	11 US-11-210-139-17	Sequence 17, Appl
35	260.5	12.6	442	11 US-11-100-640-34	Sequence 34, Appl
36	260	12.5	384	11 US-11-073-420-4	Sequence 4, Appl
37	257.5	12.4	359	9 US-10-995-561-712	Sequence 712, App
38	257.5	12.4	359	9 US-10-995-561-716	Sequence 716, App
39	257.5	12.4	359	11 US-11-127-877-65	Sequence 65, Appl
40	257.5	12.4	388	9 US-10-995-561-713	Sequence 65, Appl
41	257.5	12.4	394	9 US-10-995-561-714	Sequence 714, App
42	257.5	12.4	394	9 US-10-995-561-715	Sequence 715, App
43	256	12.3	384	11 US-11-073-420-2	Sequence 2, Appl
44	256	12.3	384	11 US-11-073-420-8	Sequence 8, Appl
45	254.5	12.3	359	9 US-10-876-787-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-10-987-856-15  
; Sequence 15, Application US/10987856  
; Publication No. US20060014242A1  
; GENERAL INFORMATION:  
; APPLICANT: WEINSHANK, RICHARD L.  
; APPLICANT: WALKER, MARY W  
; APPLICANT: BRANCHER, THERESA  
; TITLE OF INVENTION: MODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, AN  
; FILE REFERENCE: 1795/46166BZA  
; CURRENT APPLICATION NUMBER: US/10/987,856  
; CURRENT FILING DATE: 2004-11-12  
; PRIOR APPLICATION NUMBER: US/09/962,646  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/200,673  
; PRIOR FILING DATE: 1998-11-25  
; PRIOR APPLICATION NUMBER: 08/566,096  
; PRIOR FILING DATE: 1995-12-01  
; PRIOR APPLICATION NUMBER: 08/349,025  
; PRIOR FILING DATE: 1994-12-01  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 384  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-987-856-15

Query Match	16.8%;	Score	348.5;	DB	9;	Length	384;
Best Local Similarity	25.7%;	Pred. No.	1.5e-23;				
Matches	88;	Conservative	79;	Mismatches	153;	Indels	23;
Gaps	6;						
QY	18	STISNVITSHNNGSCIOIAEIAAAGDIDITVDFVIRSIFITFLVGLFVIGFGNGVL	77				
Db	3	STLFSQVENHSHVSEKNAQLLAFENDDCHLPLAMITFLAYGAVILVSGNGLAI	62				
QY	78	WAVARNKRLQSRNVLNLIPTDLILVFTAIPTVTFWYAMTKDWAFGSVCHLVPLNSNC	137				
Db	63	LIILKQKEMRNVTNLIIVNLSPDILLVAILCLPLTFVYTLMDHVVFGKAMKLNPPVQCV	122				
QY	138	SVFTVTSWLSLTALSLQKFLHINDPTKQPVSIQALAITFLIWIIVSTLINLPYLM	190				









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; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 340
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 7tm 1, 7
; OTHER INFORMATION: transmembrane receptor domain consensus sequence
US-10-055-877-340

Query Match      13.8%; Score 286.5; DB 9; Length 254;
Best Local Similarity 26.9%; Pred. No. 3.3e-18;
Matches 76; Conservative 62; Mismatches 106; Indels 39; Gaps 7;

QY 72 GNGVLMVARNKRLQSAENVFLNLIFTDLLVFTAIPVTPMYAMTKDMAGSVNCHLV 131
Db 1 GNLLVILVIRTKLRTPTNIFLNLAVADLLFLTLPPWALYLVGGDWFGDLCVL 60

QY 132 PLSNSCSVFVTSWLSATSLDKFLHNDPT--KQVSIROALAITFLIWIIVSTLINPVL 189
Db 61 GALFVNGVASYILLTAISIDRYLAIVHPLRYRRTTPRAKVLILLVWVALLSLPPL 120

QY 190 MSFEHVDGSFYVQGETPYCGHFCDEANQSNRSKIYGTVMQLQFVVPMAVITYCYFK 249
Db 121 L-FSWLR---TVEGNTTVC-----LIDFPESVRSYVLLSTLVGFVLPFLVILVCYTR 171

QY 250 ILQKYSKDMIIQNAQFCQSLTKQSDATSRKKKNYILIAMVVTFIGCWLPLTLINLVK 309
Db 172 ILRTLK-----RARSQSLKRSRSEKAKMLLVVVVFLCWLPHVILLDD 221

QY 310 DFKKEPEWLKROFFFWAINAHVIAVMSLVVW-----NPLLF 344
Db 222 SLCLLSIW-----RVLTALLITLWAVNSCLNPIIY 254

RESULT 11
US-10-877-346-83
; Sequence 83, Application US/10877346
; Publication No. US20060014153A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
```

```
; APPLICANT: Ellerman, Karen
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/10/877,346
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/964,956
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 7
; OTHER INFORMATION: transmembrane receptor Consensus Sequence
US-10-877-346-83

Query Match      13.8%; Score 286.5; DB 9; Length 254;
Best Local Similarity 26.9%; Pred. No. 3.3e-18;
Matches 76; Conservative 62; Mismatches 106; Indels 39; Gaps 7;

QY 72 GNGVLMVARNKRLQSAENVFLNLIFTDLLVFTAIPVTPMYAMTKDMAGSVNCHLV 131
Db 1 GNLLVILVIRTKLRTPTNIFLNLAVADLLFLTLPPWALYLVGGDWFGDLCVL 60

QY 132 PLSNSCSVFVTSWLSATSLDKFLHNDPT--KQVSIROALAITFLIWIIVSTLINPVL 189
Db 61 GALFVNGVASYILLTAISIDRYLAIVHPLRYRRTTPRAKVLILLVWVALLSLPPL 120

QY 190 MSFEHVDGSFYVQGETPYCGHFCDEANQSNRSKIYGTVMQLQFVVPMAVITYCYFK 249
Db 121 L-FSWLR---TVEGNTTVC-----LIDFPESVRSYVLLSTLVGFVLPFLVILVCYTR 171

QY 250 ILQKYSKDMIIQNAQFCQSLTKQSDATSRKKKNYILIAMVVTFIGCWLPLTLINLVK 309
Db 172 ILRTLK-----RARSQSLKRSRSEKAKMLLVVVVFLCWLPHVILLDD 221

QY 310 DFKKEPEWLKROFFFWAINAHVIAVMSLVVW-----NPLLF 344
Db 222 SLCLLSIW-----RVLTALLITLWAVNSCLNPIIY 254

RESULT 12
US-10-992-577-8
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; Sequence 8, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: 57155-D/JPW
; CURRENT APPLICATION NUMBER: US/10/992,577
; PRIOR FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: 09/161,113
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 8
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-992-577-8

Query Match      13.8%; Score 285.5; DB 9; Length 430;
Best Local Similarity 24.6%; Pred. No. 7.5e-18;
Matches 96; Conservative 81; Mismatches 161; Indels 53; Gaps 12;

QY 17 PSTISNVITSHNNGSCIOIAEAAQAAGIDDDITVDYF-----IRSIFFLYGFLFVLGI 70
Db 5 PSQPPNSSWPLSQNGTNTTEATPA-----TNLTFFSSYYQHTSPVAAMFIVAYALIFLLCM 58

QY 71 FGNQGVLMVAVARNKQLQSNRVFLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVNCHL 130
Db 59 VGNLTVCFLVKRHRHVTNNFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDNATCKM 118

QY 131 VPLNSCSVFTVSWSLTAISLDKFLHINDPTKQPSIROALAITFLIMVSTLINLPYLM 190
Db 119 SGLVQGMVSASVFTLVAIVERFCIVHPPEKLTLRKALVTIAVIALALLIMCPSAV 178

QY 191 SF-----EHVDGSFYVQGETPYCGHFCDEANWQSENSRKIYGTVMLLQFVVPMAVITY 245
Db 179 TLTVTREEH---HFVMDARNRSYPLYSWCEA-WPEKGMRRVYTVTLFVSHIYLAFLALIVV 234

QY 246 CYFKILQKYSKDMIIQNAQFCOSLTQ-----KORS-D--ATSRKKKNYILIAMVVTFIGCW 299
Db 235 MYATARKL-----COAPGAPGGEAADPRASRRRARRVVMVLMVVALFPTLSW 283

QY 300 LPLTLNLNVKDPKK--EPE-----WLKQRPFFWAINAHVIAVMSLVVWNPILLFFWLTRKQKR 353
Db 284 LPLWALLLLIDYGQLSAPQLHLVTVYAFPF-----AHWLAFFNSSANPIIYGTFENFR 338

QY 354 ----SGLSKILNSTEGSKAGSGLRGIQLH 380
Db 339 GFQAAFRARCLCPRPSGSHKEAYSERPGGLLH 369

RESULT 13
US-10-508-892-2
; Sequence 2, Application US/10508892
; Publication No. US20060014218A1
; GENERAL INFORMATION:
; APPLICANT: Golz, Stefan
; APPLICANT: Bruggemeier, Ulf
; APPLICANT: Weingartner, Bernhard
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
; TITLE OF INVENTION: Neuropeptide FF Receptor 1 (NPFF1)
; FILE REFERENCE: Le A 35 944
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; CURRENT APPLICATION NUMBER: US/10/508,892
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: PCT/EP03/02685
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: EP 02006654.4
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 2
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-508-892-2

Query Match      13.8%; Score 285.5; DB 9; Length 430;
Best Local Similarity 24.6%; Pred. No. 7.5e-18;
Matches 96; Conservative 81; Mismatches 161; Indels 53; Gaps 12;

QY 17 PSTISNVITSHNNGSCIOIAEAAQAAGIDDDITVDYF-----IRSIFFLYGFLFVLGI 70
Db 5 PSQPPNSSWPLSQNGTNTTEATPA-----TNLTFFSSYYQHTSPVAAMFIVAYALIFLLCM 58

QY 71 FGNQGVLMVAVARNKQLQSNRVFLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVNCHL 130
Db 59 VGNLTVCFLVKRHRHVTNNFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDNATCKM 118

QY 131 VPLNSCSVFTVSWSLTAISLDKFLHINDPTKQPSIROALAITFLIMVSTLINLPYLM 190
Db 119 SGLVQGMVSASVFTLVAIVERFCIVHPPEKLTLRKALVTIAVIALALLIMCPSAV 178

QY 191 SF-----EHVDGSFYVQGETPYCGHFCDEANWQSENSRKIYGTVMLLQFVVPMAVITY 245
Db 179 TLTVTREEH---HFVMDARNRSYPLYSWCEA-WPEKGMRRVYTVTLFVSHIYLAFLALIVV 234

QY 246 CYFKILQKYSKDMIIQNAQFCOSLTQ-----KORS-D--ATSRKKKNYILIAMVVTFIGCW 299
Db 235 MYATARKL-----COAPGAPGGEAADPRASRRRARRVVMVLMVVALFPTLSW 283

QY 300 LPLTLNLNVKDPKK--EPE-----WLKQRPFFWAINAHVIAVMSLVVWNPILLFFWLTRKQKR 353
Db 284 LPLWALLLLIDYGQLSAPQLHLVTVYAFPF-----AHWLAFFNSSANPIIYGTFENFR 338

QY 354 ----SGLSKILNSTEGSKAGSGLRGIQLH 380
Db 339 GFQAAFRARCLCPRPSGSHKEAYSERPGGLLH 369

RESULT 14
US-11-223-294-54
; Sequence 54, Application US/11223294
; Publication No. US2006003532A1
; GENERAL INFORMATION:
; APPLICANT: HINUMA, Shuji
; APPLICANT: YOSHIDA, Hiromi
; APPLICANT: HABATA, Yugo
; APPLICANT: HOSOYA, Masaki
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: Novel RFRP-3 And Its DNA
; FILE REFERENCE: 2944USOP
; CURRENT APPLICATION NUMBER: US/11/223,294
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: US/10/487,634
; PRIOR FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: PCT/JP02/08466
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: JP 2001-254826
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 54
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Human
; US-11-223-294-54
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Query Match 13.8%; Score 285.5; DB 11; Length 430;  
Best Local Similarity 24.3%; Pred. No. 7.5e-18;  
Matches 96; Conservative 81; Mismatches 161; Indels 53; Gaps 12;

QY 17 PSTISNVITSHNNGSCIQIAEAAAGIDDITVDYF-----IRSIPTFLYGLFVLGI 70  
DB 5 PSQPPNSWPLSQNGTNTETPA-----TNLTSSYYQHTSPVAAMFIVAYALIFLCM 58

QY 71 FNGGVLWAVARNKRLQSGARNVFLNLIFTDLILVFTAIPVTPWYAMTKDWAQFVGMCHL 130  
DB 59 VGNLTVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGPPFDNATCKM 118

QY 131 VPLNSCSCVFVTSWLSLTAISLDKFLHINDPTKQPVSIQALAITFLIWIIVSTLINLPYLM 190  
DB 119 SGLVQGMVSASVFTLVAIAVERPRCIVHPPREKLTLRKALFTLAVIWAALIMCPSAV 178

QY 191 SF-----BHVDSGFYVQGETPYCGHPCDEANQSENRSKIYGTVMLLQFVPMVAVITY 245  
DB 179 TLTVTREH---HFMDARNRSYPLYSCEA-WPEKGMKRVYTAFLFAHIYLVPLALIV 234

QY 246 CYFKILOKVSXDMIIQNAQFCOSLTQKORS-----ATSRKK-KVNYIILIAMVVTFIG 297  
DB 235 MYVRIARKL-----COAPGAPDTEEAEGRTISRRARVVMVLMVVALFPTL 283

QY 298 CWLPLTLNLVKDKPKBPEMLKROPPFWAINAH-----VIAMSLVVM-----NPLLPFW 346  
DB 284 SWLPLWVLLLDYGLSE-----LQLHLLSVVAPPLAHWLAFPHSSANPIIYGY 333

QY 347 LTRKQKR 353  
DB 334 FNFENFR 340

Search completed: May 8, 2006, 09:38:33  
Job time : 29 secs

RESULT 15  
US-10-992-577-2  
Sequence 2, Application US/10992577  
Publication No. US2005026087A1  
GENERAL INFORMATION:  
APPLICANT: Gerald, Christophe P.G.  
APPLICANT: Jones, Kenneth A.  
APPLICANT: Bonini, James A.  
APPLICANT: Borowsky, Beth E.  
APPLICANT: Craig, Douglas A.  
TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide PF (NPFF) Receptors  
FILE OF INVENTION: And Uses Thereof  
FILE REFERENCE: 57155-D/JPW  
CURRENT APPLICATION NUMBER: US/10/992,577  
PRIOR FILING DATE: 2004-11-18  
PRIOR APPLICATION NUMBER: US/09/538,036  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: 09/405,558  
PRIOR FILING DATE: 1999-09-24  
PRIOR APPLICATION NUMBER: 09/255,368  
PRIOR FILING DATE: 1999-02-22  
PRIOR APPLICATION NUMBER: 09/161,113  
PRIOR FILING DATE: 1998-09-25  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 432  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-10-992-577-2

Query Match 13.8%; Score 285.5; DB 9; Length 432;  
Best Local Similarity 24.3%; Pred. No. 7.5e-18;  
Matches 89; Conservative 78; Mismatches 139; Indels 61; Gaps 11;

QY 17 PSTISNVITSHNNGSCIQIAEAAAGIDDITVDYF-----IRSIPTFLYGLFVLGI 70  
DB 5 PSQPPNSWPLSQNGSDVETSNATS-----LTFSSYYQHTSPVAAMFIAAYVLIPLLCM 58

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 8, 2006, 09:33:48 ; Search time 47 Seconds  
(without alignments)  
698.346 Million cell updates/sec

Title: US-10-650-467-105  
Perfect score: 2074  
Sequence: 1 MVSSAATISTITTTPTSTI.....QLHDLPTSTHSDRCAGNSF 397

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5 COMB.pep.\*  
2: /cgn2\_6/prodata/1/iaa/6 COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/H COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/RE COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2074	100.0	397	2	US-09-721-870-105
2	2074	100.0	499	2	US-09-721-870-40
3	1859	91.6	433	2	US-09-721-870-107
4	607.5	29.3	450	2	US-09-721-870-16
5	529	25.5	600	2	US-09-693-746-2
6	515.5	24.9	376	2	US-09-721-870-22
7	485.5	23.4	457	2	US-09-721-870-26
8	461.5	22.3	365	2	US-09-721-870-36
9	460.5	22.2	387	2	US-09-721-870-14
10	458	22.1	381	2	US-09-721-870-12
11	458	22.1	402	2	US-09-721-870-8
12	458	22.1	404	2	US-09-721-870-6
13	458	22.1	406	2	US-09-721-870-10
14	388	18.7	458	2	US-09-693-746-6
15	386	18.6	370	2	US-08-513-974B-26
16	386	18.6	370	2	US-08-513-974B-323
17	386	18.6	370	2	US-09-172-353-5
18	386	18.6	370	2	US-08-776-971-21
19	386	18.6	370	2	US-08-776-971-104
20	386	18.6	370	2	US-09-799-955-5
21	386	18.6	370	2	US-09-461-438B-26
22	386	18.6	370	2	US-09-576-290-21
23	386	18.6	370	2	US-09-576-290-104
24	386	18.6	370	2	US-09-716-147-21
25	386	18.6	370	2	US-09-716-147-104
26	385.5	18.6	370	2	US-09-172-353-2
27	385.5	18.6	370	2	US-09-172-353-3

28	385.5	18.6	370	2	US-09-799-955-2	Sequence 2, Appli
29	385.5	18.6	370	2	US-09-799-955-3	Sequence 3, Appli
30	382	18.4	376	2	US-09-721-870-44	Sequence 44, Appl
31	373.5	18.0	370	2	US-09-172-353-7	Sequence 7, Appli
32	373.5	18.0	370	2	US-09-799-955-7	Sequence 7, Appli
33	371.5	17.9	369	2	US-09-170-496D-178	Sequence 178, App
34	368.5	17.8	369	2	US-09-172-353-6	Sequence 6, Appli
35	368.5	17.8	369	2	US-09-799-955-6	Sequence 6, Appli
36	368.5	17.8	369	2	US-09-170-496D-26	Sequence 117, App
37	368	17.7	434	2	US-09-721-870-117	Sequence 115, App
38	367.5	17.7	427	2	US-08-776-971-115	Sequence 115, App
39	361.5	17.4	370	2	US-08-776-971-140	Sequence 140, App
40	361.5	17.4	370	2	US-09-576-290-140	Sequence 140, App
41	361.5	17.4	370	2	US-09-716-147-140	Sequence 6, Appli
42	356.5	17.2	371	1	US-08-415-818-6	Sequence 6, Appli
43	356.5	17.2	371	1	US-08-894-236-6	Sequence 4, Appli
44	356.5	17.2	371	1	US-08-919-624-4	Sequence 6, Appli
45	356.5	17.2	371	4	PCT-US96-01444-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1  
US-09-721-870-105  
; Sequence 105, Application US/09721870  
; Patent No. 6632621  
; GENERAL INFORMATION:  
; APPLICANT: Lowery, David E.  
; APPLICANT: Geary, Timothy G.  
; APPLICANT: Kubiak, Teresa J.  
; APPLICANT: Larsen, Martha J.  
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 28341/6223  
; CURRENT APPLICATION NUMBER: US/09/721,870  
; CURRENT FILING DATE: 2000-11-24  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 105  
; LENGTH: 397  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-721-870-105

Query Match	100.0%;	Score 2074;	DB 2;	Length 397;
Best Local Similarity	100.0%;	Pred. No. 9e-165;		
Matches 397;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MVSSAATISTITTTTPTSTISNVITSHNNGSCIQIAEIAAAGIDDDITVDYFIRSIFTF	60	
Db	1	MVSSAATISTITTTTPTSTISNVITSHNNGSCIQIAEIAAAGIDDDITVDYFIRSIFTF	60	
QY	61	LYGFLVFLGIFGNGVLAARNKELQARNVFLANLFTDLILVFTAIPVTPWTAMTKD	120	
Db	61	LYGFLVFLGIFGNGVLAARNKELQARNVFLANLFTDLILVFTAIPVTPWTAMTKD	120	
QY	121	WAFGVMCHLVPLNSCSVFVTSWLSLTAISLDKFLHNDPTKQPVSIHQALAITFLIWT	180	
Db	121	WAFGVMCHLVPLNSCSVFVTSWLSLTAISLDKFLHNDPTKQPVSIHQALAITFLIWT	180	
QY	181	STLINLPLMSEPHVDGSGFYQPGTTCGHCDEANQSENRSKIYGTVMLLQFVPM	240	
Db	181	STLINLPLMSEPHVDGSGFYQPGTTCGHCDEANQSENRSKIYGTVMLLQFVPM	240	
QY	241	AVITCYFKILQKSKDMIIQNAQFCQSLTKQSDATSRKKVNVILLIAMVTFIGWL	300	
Db	241	AVITCYFKILQKSKDMIIQNAQFCQSLTKQSDATSRKKVNVILLIAMVTFIGWL	300	
QY	301	PLTLNLVKDKCKPEWLKQPFPPWAINAHVIAVSVVNNPILFFWLTRKQKRSGLSKIL	360	
Db	301	PLTLNLVKDKCKPEWLKQPFPPWAINAHVIAVSVVNNPILFFWLTRKQKRSGLSKIL	360	
QY	361	NSTEGSKAGSGLRGIQLHDLPTSTHSDRCAGNSF	397	

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361 NSTGSKKAGGSLRGIQLHDLPTSTHSDRCAGNSF 397

RESULT 2
US-09-721-870-40
; Sequence 40, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/09/721,870
; CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-721-870-40

Query Match 100.0%; Score 2074; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.2e-164;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVSSAATISTITSTTTPTSTISNVITSHSNNGSCIQAIAEAAIAAQGIDITVDYFIRSITFP 60
Db 103 MVSSAATISTITSTTTPTSTISNVITSHSNNGSCIQAIAEAAIAAQGIDITVDYFIRSITFP 162
Qy 61 LYGLFVLGIFGNGGVLWAVARNKLOARNVFLNLIFTDLILVFTAIPTVPWYAMTKD 120
Db 163 LYGLFVLGIFGNGGVLWAVARNKLOARNVFLNLIFTDLILVFTAIPTVPWYAMTKD 222
Qy 121 WAFGVMCHLVPLNSCSVFVTSMSLTASLDKFLHNDPTKQPSIRQALAITFLIWI 180
Db 223 WAFGVMCHLVPLNSCSVFVTSMSLTASLDKFLHNDPTKQPSIRQALAITFLIWI 282
Qy 181 STLNLPLMSFEHVDGSFYVQGETPYCGHFCDEANWQSENRSKIYGTVMLLQFVVP 240
Db 283 STLNLPLMSFEHVDGSFYVQGETPYCGHFCDEANWQSENRSKIYGTVMLLQFVVP 342
Qy 241 AVITYCYFKILQKVKMDIIONAQFCOSLTQKQSDATSRKKKNYILIAMVVTPIG 300
Db 343 AVITYCYFKILQKVKMDIIONAQFCOSLTQKQSDATSRKKKNYILIAMVVTPIG 402
Qy 301 PLTLNLVKDPKKEPEWLKQPPFWAINAHVIAVMSLVVWNPFLPFMLTRKQKRSGLSKIL 360
Db 403 PLTLNLVKDPKKEPEWLKQPPFWAINAHVIAVMSLVVWNPFLPFMLTRKQKRSGLSKIL 462
Qy 361 NSTGSKKAGGSLRGIQLHDLPTSTHSDRCAGNSF 397
Db 463 NSTGSKKAGGSLRGIQLHDLPTSTHSDRCAGNSF 499

RESULT 3
US-09-721-870-107
; Sequence 107, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/09/721,870
; CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 107
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-721-870-107

Query Match 91.6%; Score 1899; DB 2; Length 433;
Best Local Similarity 100.0%; Pred. No. 3.7e-150;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVSSAATISTITSTTTPTSTISNVITSHSNNGSCIQAIAEAAIAAQGIDITVDYFIRSITFP 60
Db 1 MVSSAATISTITSTTTPTSTISNVITSHSNNGSCIQAIAEAAIAAQGIDITVDYFIRSITFP 60
Qy 61 LYGLFVLGIFGNGGVLWAVARNKLOARNVFLNLIFTDLILVFTAIPTVPWYAMTKD 120
Db 61 LYGLFVLGIFGNGGVLWAVARNKLOARNVFLNLIFTDLILVFTAIPTVPWYAMTKD 120
Qy 121 WAFGVMCHLVPLNSCSVFVTSMSLTASLDKFLHNDPTKQPSIRQALAITFLIWI 180
Db 121 WAFGVMCHLVPLNSCSVFVTSMSLTASLDKFLHNDPTKQPSIRQALAITFLIWI 180
Qy 181 STLNLPLMSFEHVDGSFYVQGETPYCGHFCDEANWQSENRSKIYGTVMLLQFVVP 240
Db 181 STLNLPLMSFEHVDGSFYVQGETPYCGHFCDEANWQSENRSKIYGTVMLLQFVVP 240
Qy 241 AVITYCYFKILQKVKMDIIONAQFCOSLTQKQSDATSRKKKNYILIAMVVTPIG 300
Db 241 AVITYCYFKILQKVKMDIIONAQFCOSLTQKQSDATSRKKKNYILIAMVVTPIG 300
Qy 301 PLTLNLVKDPKKEPEWLKQPPFWAINAHVIAVMSLVVWNPFLPFMLTRKQKRSGLSKIL 360
Db 301 PLTLNLVKDPKKEPEWLKQPPFWAINAHVIAVMSLVVWNPFLPFMLTRKQKRSGLSKIL 360
Qy 361 NSTE 364
Db 361 NSTE 364

RESULT 4
US-09-721-870-16
; Sequence 16, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/09/721,870
; CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-721-870-16

Query Match 29.3%; Score 607.5; DB 2; Length 450;
Best Local Similarity 35.3%; Pred. No. 1.4e-42;
Matches 119; Conservative 76; Mismatches 111; Indels 31; Gaps 7;

Qy 33 CQIAEAAIAAQGIDITVDYFIRSITFYGLFVLGIFGNGGVLWAVARNKLOARNV 92
Db 9 CIDVNAIL--QQFNDWTVLFEVRLGYSVLFLIILIGLVNGLLTSLMRKCL--SVANI 65
Qy 93 FLNLILFTDLILVFTAIPTVPWYAMTKDQWAGVMCHLVPLNSCSVFVTSMSLTASLD 152
Db 66 FLNLINLSDLLCLCTTAVFTIPVLAFMKRWIFGIIMCKLVPTCOAFSVLISSWSLCYIAID 125
Qy 153 KFLHNDPTKQPSIRQALAITFLIWIIVSTLINLPLMSFEHVDGSFYVQGET----- 206
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Db 126 RYRSIVTPEPNSDRHARWLLMFTVVAFLASVPL-----YISQNLKMTIENV 175
QY 207 PYCHFCDEANQSENRSKI-YGTTVNLQFVVPMAVITYCYFKILQKVSMDIIONAQF 265
Db 176 TLGDCFCGFNQSDISKLTYTTSLLIIQLIIPAIMSPCYLMIQKVQTDWLVBEGSM 235
QY 266 CQSLTKQKSDATSRKKKNYILIAMVVFICGWLPLTLNLVVDKFKBEPW----- 317
Db 236 ---LTAQAQATAVRRRVNMYLILMVIFMACWFLPSAVNLFRLDGLMRPFECQTVYKVL 292
QY 318 LKQPFPMNAHVIAMSLVWNPPLFFFWLTKRQKRS 354
Db 293 MNDQWYFKLLNVHVIAMTSVWNPVLYFWMSKRRRA 329

RESULT 5
US-09-693-746-2
; Sequence 2, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; TITLE OF INVENTION: Related To The Same
; FILE REFERENCE: 6297.1cp
; CURRENT APPLICATION NUMBER: US/09/693,746
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 600
; TYPE: PRT
; ORGANISM: D. melanogaster
US-09-693-746-2

Query Match 25.5%; Score 529; DB 2; Length 600;
Best Local Similarity 30.5%; Pred. No. 6.7e-36;
Matches 136; Conservative 76; Mismatches 154; Indels 80; Gaps 12;

QY 6 AIIISITITTTST-----ISNVITSHNNGSCIOIAEIAAAGID---DITVDFY 53
Db 2 ANLSMLSTITTTSSSISTSQLPLVSTTNWLSLTPGTTSAILDVAASDEDRSGGIHNQF 61
QY 54 IRSIFFLYGLFVLGIFGNGVLMVARNKRLQSNRVFLNLIFTDLILVFTALPVP 113
Db 62 VQIFFVLYATVFLGVFGVNLVYVVLNRAMQVTNIFITNLALSDILLCLVAVPFP 121
QY 114 WYAMTKDWAFGVMCHLVPLSNCSVFVTSWLSLTALSLDKFLHNDPTKQPVSIQALAI 173
Db 122 LYTEWGRWAFGLSCLHLSFAQCSYISTLTLSAIDRYFVIYFPFPRKMLSTCIGI 181
QY 174 TFLIVSTLNLPLYMSFE-----HVDGSFYVQPG----- 204
Db 182 IVSIWVIALLATVPYGMVMTNELVNGTGTNETLVEATLMNGSFVAQSGGFIEAPDS 241
QY 205 -----ETPCGHFCDEANQSENRSKIYGTVMNLQFVVPMAVITYC 246
Db 242 TSAQYQMVMTAGTGPMPYRVYVCEB-NWPFSEQYRKVFGAITTTTLQFVLFFIISIC 300
QY 247 YFKILQKVSMDIIONAQFCQSLTKQKSDA-TSRKKKNYILIAMVVFICGWLPLTL 305
Db 301 YWISVKLN-----QBARAKPSKSSRREARDRKTRNMLIAMVAVFGLSWLPINVV 355
QY 306 NLVQDFP-KKBPWLKRQPFPMNAHVIAMSLVWNPPLFFFWLT---RKQKRSGL----- 356
Db 356 NIFDDFDKSNWRVILFFV--AHSIAMSTCYNPFYAMLENFRKFKHVLPCFNP 413
QY 357 --SKLNSTEGSKAGGSLRGIQLH 380
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Db 414 SNNINIITRGYNRSDRNTC-QPRLH 438

RESULT 6
US-09-721-870-22
; Sequence 22, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/09/721,870
; CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 22
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-721-870-22

Query Match 24.9%; Score 515.5; DB 2; Length 376;
Best Local Similarity 30.3%; Pred. No. 5.2e-35;
Matches 119; Conservative 78; Mismatches 131; Indels 65; Gaps 11;

QY 29 NNGSCIOIAEATAAAGIDDIIVDFVIRSIFTLYGLFVLGIFGNGVLMVARNKRLQS 88
Db 2 NGSDCLNLNSELWLYR-BDLSRWYIMLVFAFLYLIITAAAGIIGNSCVILATRNKSLQT 60
QY 89 ARNVFLMLIFTDLILVFTAIPTVPMYAMTKDWAFGVMCHLVPLSNCSVFVTSWLSLA 148
Db 61 VFNFLSLSCSDIVVCTSATITITAFKKEWIFGEALCRAPTAGISLCFSFTILTA 120
QY 149 ISLDKFLHNDPTKQPVSIQALAIITFLIWIIVSTLINPYLMSFPHVDSFYVQPEPTY 208
Db 121 ISIDRYILIRFPMRKPIITHYQAVGVIAITCAPAATITSPIM--FKQKLGFE-----ENF 172
QY 209 CGHFCDEANW-QSENRSKIYGTVMNLQFVVPMAVITYCYFKILQKVSMDIIONAQFCQ 267
Db 173 CQGYCTE-NWGANQSKYIGALMPLQLVPLTLIIISYTAISLKIGQSMILKGA----- 227
QY 268 SLTKQKSD-----ATSRKKKNYILIAMVVFICGWLPLTLNLVQDFPKBP 315
Db 228 ---KKQKTDNWEMLSDQORLAVKRRQRTNRMILGMVAVAFCSWISVTFNLRDYEYLP 284
QY 316 EWLKRQPFPMNAHVIAMSLVWNPPLFF-----FWLTKRQKRSGL---LS 357
Db 285 ELIKTQYIFGIATHCIAMTSTVWNPFLVAVNLQRAAFIDLMPHLLRRHLNLEGDNS 344
QY 358 KILN-----STEGSKAGGSLRGIQLHDLIP 384
Db 345 PLLNHTTMTITNKPSQ-----HTLIP 366

RESULT 7
US-09-721-870-26
; Sequence 26, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/09/721,870
; CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: Patent in Ver. 2.0
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; SEQ ID NO 26
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-721-870-26

Query Match      23.4%; Score 485.5; DB 2; Length 457;
Best Local Similarity 30.8%; Pred. No. 2e-32;
Matches 117; Conservative 69; Mismatches 117; Indels 77; Gaps 10;

QY 58 FTFLYGLFVLGIFGNGGVLMAVARNKRLQSGARNVFLNLFTDLILVFTAIPTVPMYAM 117
Db 29 FLTVFLFLFLGLFGNVTLLVVTCSHKALLSVQNFILNLAASDCMWCILSLPTITNV 88

QY 118 TKDNAPGSVMCHLVPLNSCSVFVTSMSLTALSLDKFLHINDPTKQPSIRQALAITPLI 177
Db 89 YKNMYFGNLLCHLIPCIOGISIFVCTFSIGAIALDRYILVVRPHSTPLSQRGAFLLTVLL 148

QY 178 WIVSTLINLPYLMSPEHVDGSPYQPGTPYCGHFCDEANQSENRSKIYGTVMMLQPV 237
Db 149 WILSPVVTLPYAFNMQMEYT-----EERICGYFCTE-KWESAKSRRAYTWIVMLAQPV 201

QY 238 VPMAVITYCYFKILQKQVSK-----DMIIQNA-----QFCOSLT----- 270
Db 202 VPFAMAFYANIVSVLSKRAQTKIRKAVERTSALESSCAPSHGLEQYENELNEFLDKQ 261

QY 271 QKQSDATSRKKKQVNYILIAMVVTFIGWFLPLTLNLVNDPKKEPEWLRQPPF----- 324
Db 262 EKEQRVVLQNRRTTSILVTWVWFGITWLPNHNVISLIIEYD-----DTQSFPLYGRD 315

QY 325 -----WAIN--AHVTAMSLVWNPILFFWL-----TRKQKRSGLSKILNST---- 363
Db 316 DYDISILNLPHTSHAMNNVNLNPLVYLAWNPSPQLVKTYPGDRKSDRIINGTSYVK 375

QY 364 -----EGSKKAGSGG 373
Db 376 TKIVHDTKHLNGRAKIGGG 395

RESULT 8
US-09-721-870-36
; Sequence 36, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/09/721,870
; CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 36
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-721-870-36

Query Match      22.3%; Score 461.5; DB 2; Length 365;
Best Local Similarity 30.9%; Pred. No. 1.6e-30;
Matches 110; Conservative 79; Mismatches 138; Indels 29; Gaps 8;

QY 28 SNNGSCIOIAEIAAQGIDITVDYFIRSIFTLFGFLVGLFGNGGVLMAVARNKRLQ 87
Db 2 SSSNHCIDI-RAYLWQTKHDLTHPIPIAIIATITIIIVVGVGTGMLLVMSVMRKFVLQ 60

QY 88 SARNVFLNLFTDLILVFTAIPTVPMYAMTKDAPGSVMCHLVPLNSCSVFVTSMSLT 147
Db 61 SVRNMFIVSLVSDTFVAIVSGSVPTITAFSKVMLFGGPLCHLLPLLOQTALSFSTLTIT 120

QY 148 AISLQKFLHINDPTKQPSIRQALAITPLIWIIVSTLINLPY-----LMSFEHVDGSPYVQ 202

; SEQ ID NO 121
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-721-870-14

Query Match      22.2%; Score 460.5; DB 2; Length 387;
Best Local Similarity 28.5%; Pred. No. 2e-30;
Matches 105; Conservative 80; Mismatches 118; Indels 65; Gaps 8;

QY 47 DITVDYFIRSIFTLFGFLVGLFGNGGVLMAVARNKRLQSGARNVFLNLFTDLILVF 106
Db 18 DMTNEPTVLVTFSLLYLHIFLIGILGNSAVLYLTWKHRQLQTVQNIPTNLCSNVLMLCL 77

QY 107 TAIPVTPMYAMTKDAPGSVMCHLVPLNSCSVFVTSMSLTALSLDKFLHINDPTKQPS 166
Db 78 TSLPTITFTITNYKQWFFSSPVCKLIPLVQGSIFVSTFSLSAIALDRYNLVVRPHKQKLS 137

QY 167 IRQALAITPLIWIIVSTLINLPY--LMSFEHVDGSPYQPGTPYCGHFCDEANQSENRS 224
Db 138 SRSAMMIALLIWISVVVCMYGYMDEVKING-----LCGEYCSE-HWFLAEVVR 186

QY 225 KIYGTVMMLQFVPMNAVITYCYFKI-----LQKVS-KDMIIQNAQFC----- 266
Db 187 KGYTFLVLTITQFLPPFATMAFCYVNIPTSLRQRVETKCLKLSERQLENSTTCGTNHI 246

QY 267 -----QSLTKQSDATSRKKKQVNYILIAMVVTFIGWFLPLTLNLVNDPKKEPEW 317
Db 247 VSINAEAVQNGLENKQRLAVLAQQRRTTILSCWLLFAFTWLPNNVVTLMIEY----- 300

QY 318 LKQRPFFW-----AINAHVTAMSLVWNPILFFWLTRKQKRSGLSKILN 361
Db 301 ---DGFFHSDETSATSDHTYIVSWTAHLISMLTNVTNPPFLYAWLNPMFKEMLITLGR 357

QY 362 STEGSKKA 369
Db 358 GSKSPKPA 365

RESULT 10
US-09-721-870-12
; Sequence 12, Application US/09721870
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Search completed: May 8, 2006, 09:35:08  
Job time : 49 secs

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